# User manual for Segment - Software for Quantitative Medical Image Analysis v1.8 R1172

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# 1 Regulatory status

Segment may be used for either investigational off label use or commercial purposes. Please see license terms which license form that apply to you. Users are also required to investigate the regulatory requirements pertinent to their country or location prior to using Segment. It is in the users responsibility to obey these statues, rules and regulations.

## 1.1 Commercial usage of Segment

FDA approved versions of Segment are identified with a labelling upon start up displaying licence details and the FDA 510(k) number K090833. If your version does not display this information your version is not FDA approved and you need to contact Medviso AB to receive a such license.

Please note that there are features that are not included in the FDA approval. These functions are marked in the user manual with *'The functions described in this chapter is off label use and for investigational use only.'*

### 1.1.1 Indications for use

Segment is a software that analyzes DICOM-compliant cardiovascular images acquired from magnetic resonance (MR) scanners. Segment specifically analyzes the function of the heart and its major vessels using multi-slice, multi-frame and velocity encoded MR images. It provides clinically relevant and reproducible data for supporting the evaluation of the function of the chambers of the heart such as left and right ventricular volumes, ejection fractions, stroke volumes, peak ejection and filling rates, myocardial mass, regional wall thickness, fractional thickening and wall motion. It also provides quantitative data on blood flow and velocity in the arterial vessels and at the heart valves. Segment is tested on MR images acquired from both 1.5 T and 3.0 T MR scanners. The data produced by Segment is intended to be used to support qualified cardiologist, radiologist or other licensed professional healthcare practitioners for clinical decision making. **It is a support tool that provides relevant clinical data as a resource to the clinician and is not intended to be a source of medical advice or to**

**determine or recommend a course of action or treatment for a patient.**

## 1.2 Investigational purposes

None of the organizations/persons named in conjunction with the software can accept any product or other liability in connection with the use of this software for investigational purposes

# 2 License Terms

The software can be used under three different license forms. More detailed information and pricing of the different license forms is given on Medviso AB homepage `http://www.medviso.com`.

## 2.1 Free or charge for non-commercial research

The software is free to use for non-commercial research or educational purposes if and only if you reference it properly and send full bibliographic information (such as Pubmed link) of your final work when published or accepted for publication. Details on how to reference the software are given in Chapter 28.

You may not use the software for clinical routine or commercial applications such as company paid pharmaceutical trials without contacting the author. Details about commercial/clinical use is given below. Note that the software is copyright and may not be redistributed/resold without permission of the author.

## 2.2 Commercial or Clinical use

To use the software for clinical routine or commercial research (see above) you need a commercial license of Segment. Details on how to acquire a such license and prices are found on the homepage `http://www.medviso.com`. This version of Segment is FDA 510(k) approved, K090833. The license includes some extended functionality in forms of different modules that are not available in the free research only version. Depeding on the exact configuration your commercial version may include some or all of the following extra features.

- Support! Details about the support is given in Chapter 30.
- Report sheet generator. In this module it is possible to print a report sheet with a results and free text annotations as a patient report. This is described in Chapter 41.

- Native Bruker file format reader. The Native Bruker file format support module allows you to directly load Bruker files into Segment. This is described in Chapter 36.
- Segment patient database. This allow you to easily find and load your patient images. This module is further described in Chapter 37.
- Segment DICOM server module. This module allows Segment to work as a standalone workstation and receive images directly from the scanner, a hospital PACS, or another DICOM workstation. This module is further described in Chapter 38.
- Segment PACS connection module. This module allows you to download and export images directly to a PACS system. This module is further described in Chapter 39.

## 2.3 Commercial research (non-human images)

There is also a non FDA approved version for commercial purposes of Segment available. This license type is intended for commercial R & D companies, or industry sponsored trials where the majority (more than 50%) of the funding comes from a commercial sponsor.

## 2.4 Future modules

Then there are also a few modules that are not yet available to the research community, but will be made freely available when we have published methods paper describing the adequately.

- Strain analysis from velocity encoded MRI images.
- SPECT Module, including automated LV segmentation of gated images, and perfusion defect size estimates.
- Sectra Plug-in Module. This will allow you to run Segmentas a plug-in to Sectra PACS.
- T2* Module.
- Image Fusion Module.
- Automated whole heart segmentation of CT images.
- Automated bone segmentation of CT images.

- Volume Rendering Module.
- ...

# 3 Acknowledgements

Even if this project started as a one man project, it has grown and it would never been possible without the help of many many people.

Financial support has been received from the Swedish Heart-Lung foundation, Swedish Research Council, local founds from Östergötland County, and Region of Scania.

I would like to acknowledge all the people that have put in feed back on usability and desired functionality, algorithm etc. Among others: Andreas Otto, Andreas Sigfridsson, Erik Bergvall, Erik Hedström, Henrik Haraldsson, Henrik Engblom, Håkan Arheden, Jan Engvall, Lars Wigström, Lisa Hård af Segerstad, Karin Markenroth Bloch, Marcus Carlsson, Martin Ugander, Mikael Kanski. Finally thank to you all Segment users in the research community that has inspired and contributed to the development.

Special thanks to code providers Erik Bergvall (core routines of strain analysis), Helen Soneson (strain analysis module, SPECT module, Image fusion module), Shruti Agarwal (refactory of strain analysis module), Jonatan Wulcan (Sectra Plugin module and general improvements), Johannes Töger (3D flow and volume tracking), Mårten Larsson (3D flow and kinetic energy).

Commercial development has been done by Jane Sjögren (improvements to general object segmentation, implementation of prototype based segmentation, CT functionality, and graphical seriesselector). General debugging and implementation of the new interpolated contours has been done by Johan Ugander and Erik Södervall.

# 4 Rationale for the Software

Developing this software have required a lot of work. So what has the rationale been for producing new software where there are commercially available software packages that at least partially could do the same thing?

- At the time of writing the core of the program other existing software were simply not good enough.
- Existing software packages did not allow to store the segmentation and regions of interest in a flexible way.
- Existing software packages had no flexible exporting capabilities to allow full usage of automated delineation algorithms.
- A freely available software greatly facilitates and improves possibilities to do multi-center studies.
- There will be no company secrets we will always know, and be open and tell you exactly how things are implemented. This is crucial for doing good research.
- It can serve as a platform for experimenting and testing of various image processing ideas.
- It has been given very valuable experience of how to handle and develop a large scientific software package.

As the software grew in capabilities, there also started to be a commercial interest in the software. However, Segment will always be tightly coupled to cardiovascular research and continue to be freely available for research purposes. We hope that you will find the software useful in your research, and please do not hesitate to tell us what you think about it, and come with suggestions for improvements.

The software has been developed at:

- Home during late evenings and weekends.
- Linköping University, Sweden, Centre of Medical Image Science and Visualization & Department of Medicine and Care, Clinical Physiology (2002-2004).

- Cardiac MR Group, Lund University, Department of Clinical Physiology (2005-present).
- The company Medviso AB (2007-present).

# 5 How to Read This User Manual

Technical documentation always face a certain dilemma: whether write for top-down or bottom-up learners. A top-down learner prefers to read or skim documentation, getting a large overview of how the system works; only then does she actually start using the software. A bottom-learner is a 'learn by doing' person, someone who just wants to dive into the software and figure it out as she goes, referring to book sections when necessary.

This documentation is biased towards top-down learners (And if you're actually reading this section, you're probably already a top-down learner yourself!) However, if you're a bottom-up person, don't despair. If you have patience enough to ready only one chapter then read Chapter 10. If you then get stuck you may use this user manual to search for specific solutions. Most of the icons and pushbuttons in the software have tooltip strings attached to them. Simply point the mouse over a button and you will have feeling on what purpose it has.

If you do not want to read the user manual at all, you can instead see the on-line video tutorials. They are available under the Help menu.

# 6 Conventions and Abbreviations

This chapter describes the typographic conventions and used abbreviations in this manual and in the program.

## 6.1 Typographic conventions

| | |
|---|---|
| `A` | Key `A` at the keyboard. |
| `Ctrl-A` | Control key. Hold down `Ctrl` key and `A` simultaneously. |
| | Icon in toolbar. |
| `*.tif` | Filename extension. |
| `C:/Program` | Folder. |
| File | Menu, i.e File menu. |
| File→Save As | Sub menu, i.e under the File menu the item Save As is found. |
| Close | Push/Toggle button in the graphical user interface. |
| ◎ Endocardium | Radiobutton in the graphical user interface. |
| ☒ Single frame | Checkbox in the graphical user interface. |

## 6.2 Abbreviations

| | |
|---|---|
| 2CH | Two chamber view |
| 3CH | Three chamber view |
| 4CH | Four chamber view |
| 3D | Three Dimensional |
| 3D+T | Time Resolved Three Dimensional |
| AA | Ascending Aorta |
| ASW | Anterior Septal Wall Thickness |
| ARD | Aortic Root Diameter |
| BPM | Beats per minute |
| BSA | Body Surface Area |
| CO | Cardiac Output |

| | |
|---|---|
| CT | Computed Tomography |
| DA | Descending Aorta |
| DE-MRI | Delayed Enhancement MRI |
| ED | End diastole |
| EDD | End Diastolic Dimension |
| EDL | End Diastolic Length |
| EDV | End Diastolic Volume |
| EF | Ejection Fraction |
| ES | End systole |
| ESD | End Systolic Dimension |
| ESL | End Systolic Length |
| ESV | End Systolic Volume |
| FWHM | Full Width Half Maximum |
| GUI | Graphical User Interface |
| HR | Heart Rate |
| LV | Left Ventricle |
| LVM | Left Ventricle Mass |
| MO | Microvascular obstruction |
| MB | Mega Byte |
| MIP | Maximum Intensity Projection |
| MPR | Multiplanar Reconstruction |
| MR | Magnetic Resonance |
| MRI | Magnetic Resonance Imaging |
| PET | Photon Emission Tomography |
| PER | Peak Ejection Rate |
| PDW | Proton Density Weighted |
| PFR | Peak Filling Rate |
| PLW | Posterior Lateral Wall Thickness |
| ROI | Region Of Interest |
| RV | Right Ventricle |
| RVmaj | Right Ventricle Major Axis |
| RVmin | Right Ventricle Minor Axis |
| SPECT | Single Photon Emission Computed Tomography |
| SSFP | Steady State Free Precision |
| SV | Stroke volume |
| TOF | Time of Flight |
| VENC | Velocity Encoding limit |

## 6.3 Trademarks

Below are some of the trademarks used in this user manual.

- Segment is a trademark of Medviso AB.
- Matlab is a trademark of the Mathworks Inc, (`http://www.mathworks.com`).

# 7 System Requirements

In this chapter the hardware requirements for the software are outlined. Possible bottlenecks are (in order of likelihood) lack of RAM memory, CPU speed, and I/O network or disk transfer rates.

## 7.1 Operating system

Segment is available both as a precompiled application and also a source code version. Precompiled versions are available for the following platforms:

- Microsoft Windows. It will run on any of the following Windows 2000, Windows XP (32 bit), Windows Vista (32 bit). At the current writing we have limited reports whether it works on Windows 7 or not.
- Microsoft OS X. It is known to work with Mac OS X 10.6.5. Many users have reported problems with Mac OS X 10.5.8. Furthermore, Segment have been reported to run well on Mac using Parallels.

The source code version is available for the following platforms:

- Windows 32
- Windows 64
- Linux 32
- Linux 64
- Mac OS X (32 bit Matlab)

To run the source code format you need Matlab R2008a or later.

## 7.2 Hardware requirements

The list below are the recommended hardware requirements. To run a clinical versin of Segment you need at least the specifications indicated below.

- A computer with at least a Pentium III processor running at 800MHz. Computers with 1.5GHz CPU speed or more are recommended. In practice this means that almost all machines purchased under 2005 or later will do.
- Harddisk with at least 500 MB of available space. The program Matlab Component Runtime takes about 450 MB, another 20MB is taken by the program.
- At least 512 MB of RAM memory, 1024 MB or more is strongly recommended. The more the merrier.
- Graphics card supporting both DirectX and OpenGL (hardware accelerated) is recommended. Systems with two screens is recommended for clinical / commercial usage of Segment.

# 8 Installing and Uninstalling

For information on how the latest version can be downloaded, see Segment homepage (`http://segment.heiberg.se`) for research only version and see distribution e-mail for commercial users.

The installation descriptions divided into three main sections, describing Windows standalone installation, Mac OS X installation, and source code installation, respectively. The sections in this chapter after that describes general settings that should be performed regardless of installation type.

## 8.1 Installation of Standalone version for Windows

This section is written for first time installation of Segment. For upgrading, see the Section 8.5. The program is written in Matlab, in order to run it you therefore need to install MatlabComponent Runtime first. **Note** that to be able to perform these steps below you **need** to have administrator privileges on the machine. If you are using Windows Vista, then please also refer to Section 8.1.5.

### 8.1.1 Installing Matlab Component Runtime

If you have Matlab **and** MatlabCompiler installed on your computer this step may not be necessary, provided that you have exactly the same version as used for compiling Segment. Currently Matlab Component Runtime 7.8 is required. Download the file `MRCInstaller_v7p8.exe`. Download the file to a suitable location (i.e your desktop or a temporary folder) and double-click it. Follow the instructions.

This step does only need to be performed once and should generally not be necessary when upgrading to a later version of the software.

### 8.1.2 Installing Segment

Download the file (called something like `install_segment_1pxRyyyy.exe`, where `1px` is the version number and `yyyy` is the revision number). Place the file where you easily can find it (i.e your desktop). When downloaded, double click on the file, and follow the instructions. You will be prompted if

you want to install the program to the default location ( `C:/Program Files` or `C:/Program` depending on operating system language). One advantage to install to a other location where you have write access is that you can thereafter install upgrades without being logged in as local administrator.

### 8.1.3 Installing Example Patient Database

If you wish to install the patient database, download the file called something like `installdatabase_v1pxRyyyy.exe`. The patientdatabase is not updated with every release of Segment and will typically only be updated for each major upgrade of Segment.

### 8.1.4 Create shortcut

Place a shortcut to the file `c:/Program Files/Segment/segment.exe` at your desktop. Note that depending on your system locale, or if you have installed Segment to a non-default location this path may be different. Creating this short-cut is done by using the standard Windows file explorer to find the file, then right click on the file and select the option Create a short-cut. Move the created shortcut to your desktop.

### 8.1.5 Notes for Windows Vista users

You will need to run the application in administrator mode the first time you run Segment since the first time Segment is started some files are extracted. This operation is blocked in user mode. The second time you run Segment you should be able to run in a user mode.

### 8.1.6 Network installation of Segment

For advanced users and system administrators, it is possible to make a network installation of Segment. Then you do not need to install MCRInstaller on each machine that is used to run Segment. Make a network installation of MCRInstaller. How to do this shown in this document.

```
www.mathworks.com/access/helpdesk/help/toolbox/compiler/f12-1000291.html
```

Thereafter place Segment in a network folder, and make sure that each user can find `segment.exe`.

## 8.2 Installation for Mac OS X

1. Download MCRInstaller file (see download pages). Double click to install it.

2. Download Segment .zip file (see download pages).

3. Place it on your desktop. Unzip the file by double click it.

4. Rename the newly created folder to Segment (**Note:** important otherwise short-cut will not work).

5. In the folder find the file "Start Segment" (an Apple script file). Drag this file out to your desktop.

6. Drag the renamed Segment folder to "Program" folder on your MAC. (That is technically `/Applications folder`).

Start Segment by click on the icon "Start Segment" on your desktop.

## 8.3 Installation for source code version

Install Segment by:

1. Download .zip file (see download pages)

2. Unzip the file and store contents in directory.

3. Installation complete.

Starting by:

1. Start Matlab

2. Change directory to where you have unpacked Segment.

3. Type segment at Matlab command prompt.

## 8.4 License file

If you have received a license file (then your version is registered full version), then copy your license file to the same folder as where segment is installed. The license file is called `yourname.key` or `license.key`. If you do not have a license file then the program will run in 'Research only mode', fully functional where only a few options are disabled. You may then **not** use the software for commercial research or clinical routine.

## 8.5 Upgrading Segment

In most cases upgrades is very simple, just download the installation file and double click on it to install it. To see which Matlab component runtime are required, please see the table below.

| **Version** | **MCRInstaller** |
|---|---|
| $\leq$1.675 | Matlab Runtime Component 7.6 |
| 1.8 - current | Matlab Compiler Runtime 7.8 |

If your previous version used another MCR then you need to **first** replace your old MatlabComponent Runtime. It is **important** to uninstall the old MCR before installing a new one. When having problems installing or uninstalling the MCRInstaller, please consult Mathworks support pages, and search for `MCRInstaller`.

## 8.6 Setting preferences

It is recommended to set the preferences of which folders to use to avoid browsing each time you want to load or save a file. It is invoked by using the Preferences on the main menu. Set `Data` and `Export` folders. Further details on how one customizes Segment is given in Customization Chapter in Segment User Manual.

### 8.6.1 Setting window positions

The position of the main window for Segment can be set by dragging the window to an optional position and size. The size and position will be saved so that next time Segment is launched the same position will be used. The window position can also be saved for the file loader, general segmentation

module, patient database module, PACS connection module, fusion module, SPECT module and strain module. This feature is under development and eventually it will be possible to set the position for all windows, until then windows will pop up as an overlay in the middle of the window from which it was launched or in the middle of the main Segment window.

In case where one have switched to another monitor Segment may move outside the screen. In this case you could press `Shift-Ctrl-R` to reset GUI positions. This is also available under the File menu.

## 8.7 Uninstallation

Essentially the uninstallation is similar for all three kinds of versions.

### 8.7.1 Uninstalling for Windows

There is currently no uninstallation software available. Remove all files in the folder `C:/Program/Segment` or `C:/Program Files/Segment`. User preferences are stored in the `Application Data` and the subfolder `Segment` under each user account (Windows). To uninstall the Matlab Component Runtime, use the Windows functionality Install or Remove Programs in the control panel menu.

### 8.7.2 Uninstalling Segment (Mac OS X)

There is currently no uninstallation software available. Remove the Matlab Component Runtime and all files associated with Segment.

### 8.7.3 Uninstallation for source code

The uninstallation for the source code version is trivial, simply delete all Segment related files.

## 8.8 Trouble shooting

The absolutely most common problem is the failure to not login as a local administrator of the computer. The second most common mistake is not to read the installation instruction provided in this user manual or on the homepage.

To trouble shoot the installation you can see if the Segment installation program actually was successfully started by checking for the existence of `.log` files. Segment creates a log file during installation, this file is stored in the user folder (i.e `Documents and Settings/Username` and `Application Data` and the subfolder `Segment`. Note that this folder by default is hidden. If you have problems installing Segment, please send this log-file to `support@medviso.com` together with a description on what problems where encountered.

# 9 Loading Image Stacks

The program can read DICOM, and also an internal file format. The internal file format (called `.mat` files) has the advantages that one file may contain several image stacks along with object contours and measurements, and it is also much faster and easier to load compared to loading DICOM files.

If you have the clinical version of Segment loading files are then better described in Chapter 37.

For research use it is highly recommendable that when an image stack has been loaded from DICOM files to save the image stack(s) to the internal file format. This makes it then much easier to go back and reanalyse datasets if necessary. Note also that the internal file format requires much less storage space that the original DICOM files, mainly due to cropping of the images and to lossless compression.

How to browse your DICOM data in the easiest way is described in Section 9.1.6.

The file loading dialog box is started from the main menu, under File, or by clicking on the icon , or by pressing `Ctrl-O`. This brings up the file loader GUI shown in Figure 1.

The file loader process the selected directory and its subdirectories to find the number of files in that directory. Since this process takes some time this operation is cached, and creates a file called `folders.cache`. To recreate the cache, press . When reading from a CD-ROM it is recommendable to copy the CD-ROM to your hard drive if you will load most of the files on the CD-ROM, since random file access from CD is very slow and caching is not possible. For further details on how to import DICOM CD-ROM's, see Section 18.5.

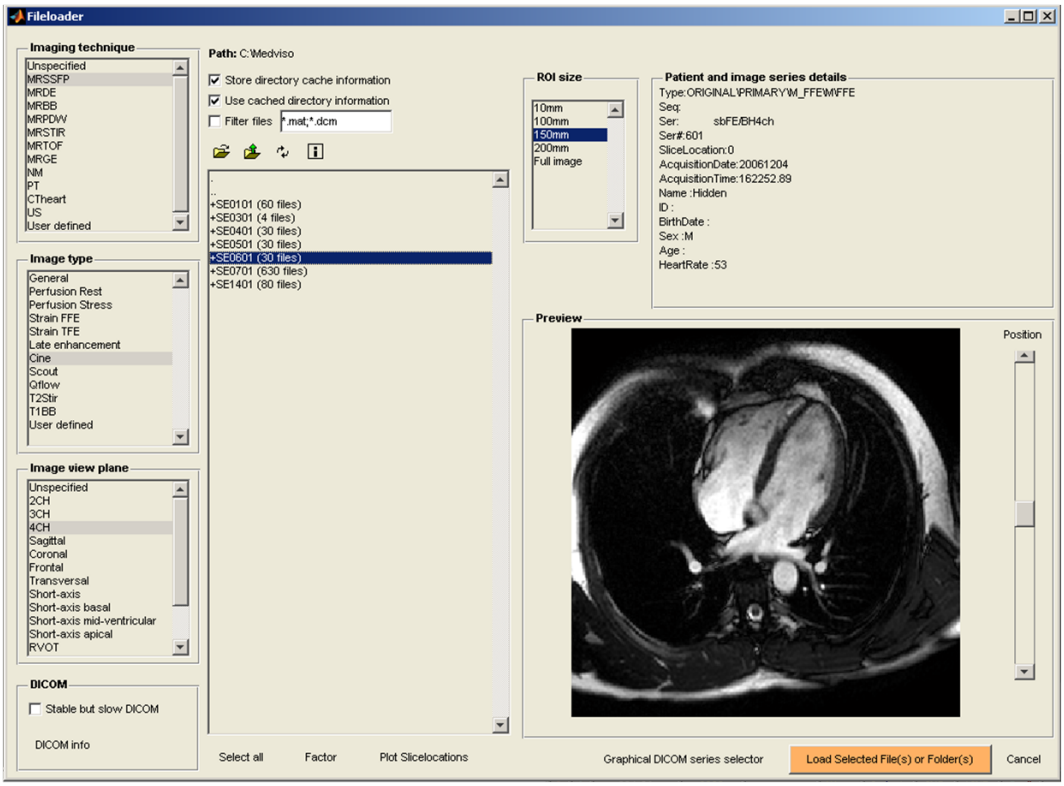



Figure 1: File loader GUI.

## 9.1 Loading DICOM files

### 9.1.1 Loading MR DICOM files

When loading MR DICOM files Segment assumes that the files are sorted so that each image series is stored into one folder. Each folder may then contain one or many DICOM files. This is illustrated in Figure 2.

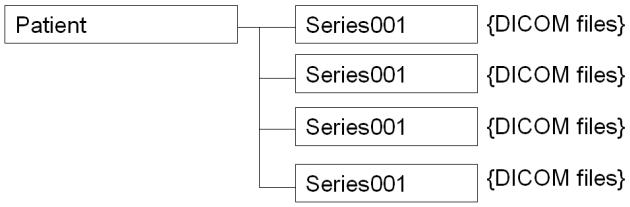



Figure 2: Files needs to be sorted so that each image series are stored into a separate folder.

If the files are not stored in this fashion then there is a sorting utility available described in Chapter 18. DICOM is an loosely structured file format and direct reading from DICOM files is slow. Currently the use of meta DICOM files is not supported (the DICOMDIR file is simply ignored). Segment therefore caches the DICOM tags in a file called `dicom.cache`. When loading files Segment by default creates a DICOM cache file so that the DICOM images can be loaded faster the next time. When retrieving images from PACS this caching operation is done at the same time as the images are downloaded. You can also start the caching operation for a folder and its subfolders, for more details see Section 18.6. This is highly recommended to do if you have a large image material with many patients that you need to analyze.

### 9.1.2 Loading SPECT DICOM files

When loading SPECT DICOM files Segment assumes that the files are reconstructed.

### 9.1.3 General loading DICOM files

You can either load each image series at a time or use a graphical tool to select what image stacks to load. The graphical series selector is described in Section 9.1.6. To load on image series at a time, start by selecting one folder. To go up one directory level double click on .., or click on the icon. To more easily get to a different folder, click on the Browse pushbutton. To go down one directory level double click on the folder name. Once selected one folder containing DICOM files a preview of one file in that folder is shown. To load the complete image stack, perform the following steps:

- Start by selecting the imaging technique in the top left corner of the GUI. The imaging technique sets the default segmentation parameters, and it is crucial that you select the correct imaging technique. For many scanners and sequence types this is identified automatically.
- When a valid file/folder is selected a preview of that dataset is displayed. Patient details and acquisition time are also shown.
- It is recommended, but generally not required to select `Image Type` and `Image View Plane`. This tells Segment what kind of image it is. This might be required for future analysis in some applications. It is also a good idea to label image stacks upon loading when for instance doing stress analysis to be able to safely differentiate baseline from stress exams. For research purposes it is possible to set free text name as `Image Type` and `Image View Plane`.
- Select the desired region of interest size. Usually for normal hearts 100mm is sufficient to cover the left ventricle. Enlarged ventricles will need 150mm or even more.
- Click Load to start the loading process. This brings up a red box in the preview image. Position this box with the mouse and left click to start the loading process. If you want to use a different size of ROI right click to abort loading operation. Then click again on the Load button.
- Once positioned the box, left click with the mouse to start loading the files.

Once all image files are loaded a dialog box opens where you need to confirm voxel spacing and timing details. An example of this confirm dialog box

is shown in Figure 3. How Segment interprets the DICOM information to calculate these parameters is described in Section 27.3. For users that do not use images from the three major vendors Siemens, Philips, or GE should read this section. Further technical details about how Segment interprets the DICOM files are given in the Application Programming Interface manual. The the files are loaded you are prompted to verify the following information:

- Number of slices (`NumSlices`).
- Number of time frames (`NumTimeFrames`).
- Time increment in ms between each time frame (`TimeIncrement`).
- Slice thickness in mm (`SliceThickness`).
- Gap between slices in mm (`SliceGap`).
- Pixelspacing in X-direction in mm (vertical direction in Segment)
- Pixelspacing in Y-direction in mm (horizontal direction in Segment)
- Velocity encoding (VENC) in cm/s. For non velocity encoded images this should be 0.
- Rotated image stack. This should by default be false. If your image stack is rotated, then change this to true.
- Cyclic image. If the image stack is cyclic, i.e covers the whole heart cycle this should be true (default). For prospectively gated image series this should be false. This affects mainly the automated segmentation algorithm.

It is very important that all these parameters are correct. If you find image stacks where the automated calculation of the above parameters fails please report this!

If heart rate is not present in the DICOM file Segment tries to guess that based on the time increment and the number of time frames to get R-R interval. This will fail if your image sequence is for instance one image every heart beat.

### 9.1.4 Tips and tricks

Often the files are not stored exactly as prerequisited above, then there are many tips and tricks available.

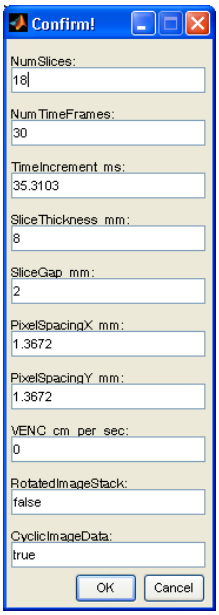



Figure 3: Confirm dialog box when finished loading an image stack.

- You may select several subfolders. Then the program loads all the files in the subdirectories. Each subdirectory must have the same number of files. This is the case for old Siemens files and Bruker Paravision DICOM files.
- You may select what DICOM files to load directly. Note however that the files need to form a valid image stack and the result may be incorrect if slices are missing etc. When you do this, always ensure that the files are sorted properly.
- It is possible to preview different files by the `Position` slider.
- To get detailed information about DICOM tags in the files press DICOM info.

### 9.1.5 Loading images from CD

When loading images from a CD it is highly recommended to import the files from the CD to your image data directory. This is done by using the utility described in Section 18.5.

### 9.1.6 Graphical image series selection

The graphical series selector tool is shown in Figure 4. While moving the mouse pointer over the image series more information on each image series is shown in the top of the graphical interface. Select which image series to load with left mouse button. Image series outlined in yellow are selected. It is also possible to group image series to one image stack. Image series that are to be grouped are selected with holding down the `Shift` key and mouse click. Thereafter, press the pushbutton Group Selected. Grouped image stacks are shown with a green outline. When finished selecting image series, press Load. To speed up the process this operation the generation of the thumbnails is cached.

Note that when using this tool to load the image, then there is no cropping of the images done, and that is highly recommended to crop the images during the image analysis process. Also note that if multiple directions is detected in the dicom folder all the different directions are loaded as separate image stacks.

### 9.1.7 DICOM - details

First of all remember that DICOM is not a well defined standard. I have tried hard to make Segment to work with DICOM files from different imaging device manufacturers. It is currently tried on General Electric MR-scanners, Siemens CT/MR/PET, and Philips MR scanners, Bruker MR, Suinsa PET. Furthermore various PACS manufacturer might 'corrupt' the files in different ways.

The DICOM reader comes in two flavors, one fast mode that tries to implement the DICOM standard in the simplest way possible. Limitations of the fast reader are no JPEG encoded images, no Big-Endian DICOM files. The stable reader tries to implement things more according to the 'standard', supporting JPEG encoded images. The stable reader does **not** support correct loading of velocity encoded image stacks. The two different flavors are chosen in the file loader GUI with the checkbox ☒ Stable but slow DICOM.

There are some short cuts taken in the fast loader:

- The spacing in time is assumed to be equal between all frames when

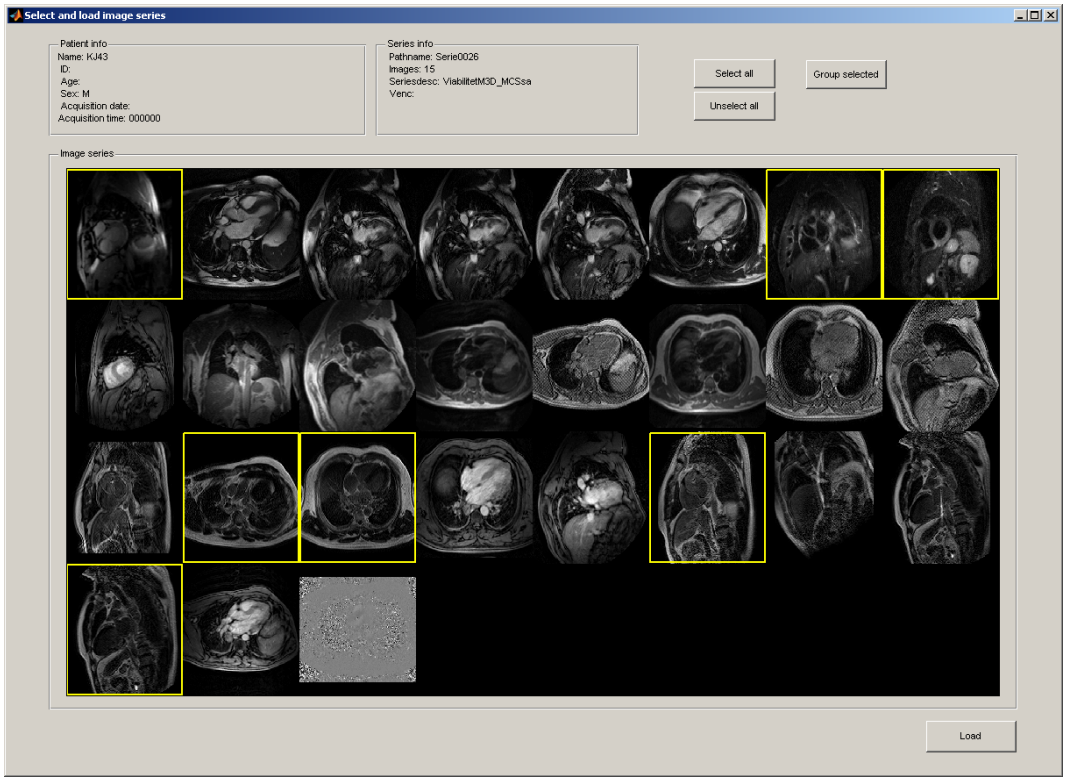



Figure 4: Graphical image series selector.

loading time resolved images. This may be violated if the scanner rejects some beats in a perfusion image serie for instance.

- The spacing in slice is assumed to be equal between all slices when loading image stacks with multiple slices.
- When you have loaded a rotated image stack you need to tell Segment about it. It is done under Image Tools and View Adjust and Image Details. A rotated image stack is a set of slices that are rotated around a central axis. Then subsequent analysis will assume that the data is a rotated image stack. When you view the data in single slice view ☐ a cyan line are drawn with the rotational axis indicated. To get correct volume estimates it is crucial that this line co-incides with the true axis of rotation. To achieve this you may have to flip the image stack, see details in Section 15.7.

### 9.1.8 Unstructured files

Some systems (Siemens depending on platform version, or how you do it or what PACS you are using) outputs files in a completely unstructured way (all patients and all time frames, and all slices) are mixed into the same folder. In Segment there is a sorting utility that can be accessed on the main menu that can sort the files. This is described in Chapter 18.

## 9.2 Matlab format - details

Internal format used by the program. The image needs the be stored in the variable `im` or `setstruct`, and must be in single precision format. The dimensions must be $x, y, t, z$. If you do not have time resolved data make sure to make the temporal dimension singleton, i.e. always put in a 4D-array. It is possible to also give dimensions, and patient specific information as well as a preview image. To learn about this, load an image stack from DICOM images, and select Save Both Image Stacks and Segmentation As under the File menu. Then load the file in Matlab, and study the variables in the file. Details about the file format is given in the Application Programming Interface manual.

# 10 Program Overview

This chapter provides an overview of the program. Another good method to get an overview of the program is to read the example in Chapter 24. Yet a good method is to view the on-line video tutorials. The tutorials are available under the Help menu.

An example of the main graphical user interface is shown in Figure 5. The major portion of the user interface is occupied by a viewing area where multiple image stacks can be visualized side by side. The current active image stack is outlined with an orange thick line. To make another image stack active, simply click on the image stack with the mouse pointer. A thumbnail image is shown for each loaded image stack. To view an image stack drag the thumbnail down to the main viewing area. To scroll through the thumbnails either use the slider or press `Ctrl` while scrolling with the mouse wheel.

The upper right corner is occupied with a reporting panel where quantitative details about the current image stacks are shown. There are two rows of icons. The top row contains icons that applies to all loaded image stacks, whereas the bottom row contains icons to applies to the current active image stack only.

Middle right part of the user interface is occupied by a volume curve and a time indicator. This graph area shows left ventricle volume versus time (red), left ventricle muscle volume (green), papillary muscle volume (blue). One easy method to adjust the displayed time frame is by clicking in this graph. You can also interactively drag which time frame that is taken as end diastole (ED) or end systole (ES). Just above the volume graph a list box with assumed long-axis motion is located. In this example the long-axis motion is automatically calculated under the assumption that the left ventricular mass is constant over time. The program selects the long-axis motion amplitude that best fits this assumption. Note that this auto detect should be disabled when manually drawing contours. For further details, see Section 11.1.2.

If the checkbox ☒ Single frame is selected then segmentation and other operations such as translate, scale, and delete are only applied to the current time

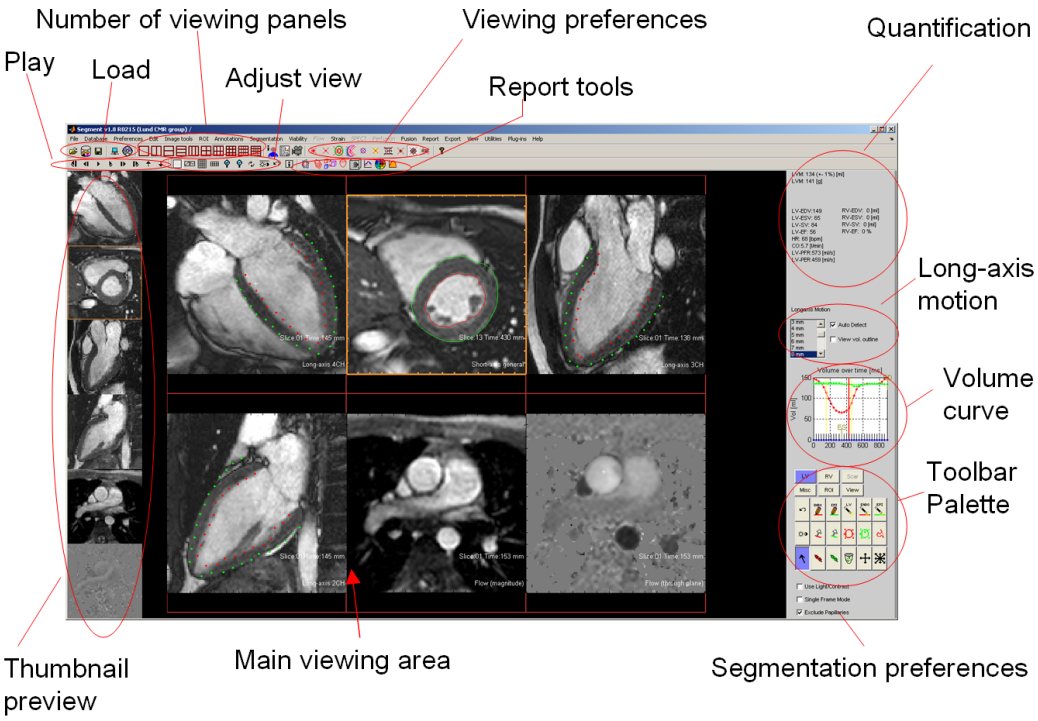


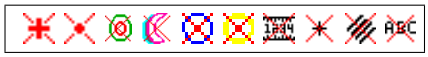

Figure 5: Main graphical user interface.

frame. To further make the user aware of this change of behavior the box around the currently selected image panel turns to white when single frame mode is selected.

## 10.1 Viewing image stacks

To view a non visible image stack simply drag the thumbnail to an image panel. Right clicking on the thumbnails brings up a context menu where more options are available. To view all loaded image stacks press `Shift-A`. Only one of the image stacks are active at the same time. Around the active image stack an orange rectangle is drawn, both in the main image drawing area, and around thumbnail image.

Image stacks can be viewed in four different modes; one slice view, montage view, montage view in rows, and m-mode view. The different modes are selected with the icons (one slice), (montage or all slices), (montage view in rows), and (m-mode view). Each of the different viewing modes will be described in details below. It is possible to view the same image stacks in different viewing modes simultaneously. The number of image panels can be selected by the icons or under the View menu. The icon views information about the patient. It also also possible to enter/adjust the patient information. Commonly this is used to add patient length to be able to calculate BSA.

The section  controls the visibility of pins, contours from other image stacks, endo / epicardium contours, region of interests, delineated infarct regions, measures and annotations, center point, and image plane intersections, respectively. The icons and  zooms in/out the current active image stack. The icon refreshes the screen which might be very useful since it also refreshed the GUI which under certain circumstances might 'hang' in case of calculations that went wrong. If the GUI seems irresponsive it is well worth to try refresh the screen. The icon resets the light/contrast setting. The icon automatically sets which sets contrast and brightness so that an upper and lower percentile of the intensities get saturated. The icon undo the latest contour editing command. The icon  shows information about the current image stack.

## 10.2 Montage view

Figure 6 shows a screen-shot of the program in the most common view (montage view), selected by the icon . You can also switch between the montage view and the single slice view by using the hot key `v`. In the montage view all slices in an image stack are displayed. The slice(s) with a yellow box around are selected. Automated segmentation and many other operations are only applied to selected slices. Slices are selected by activating the tool , and by left mouse click on the desired slice and drag the mouse while the left button is hold down.

## 10.3 Montage row view

The montage row view is same as the montage row, but with the difference that the slices are shown to minimize the number of rows that are used to display the entire image stack.

## 10.4 One slice view

In one slice view only one single slice are shown at a time. You can then browse between slices by up/down arrow keys. Right and left keys displays next and previous time frames. In this view intersecting image planes that also are shown. The intersection are indicated with a white or an orange line. Orange line indicate intersection with the current active image panel. To hide/view the plane intersections use the icon . In this view intersections with contours drawn in other image stacks are also shown. For instance if the short axis stack is segmented the contour will also be visible in the long axis image. This is illustrated in Figure 7. This is very useful to delineate structures that might be difficult to see in only one image plane. The contour intersections can be hidden by using the icon . The contour intersections are only visible in one slice view mode. Note that different breathing position may cause the image stack not to align properly.

## 10.5 M-mode view

Another viewing option is the (M-mode). Example of this view is shown in Figure 8. The viewing option is chosen by the icon .

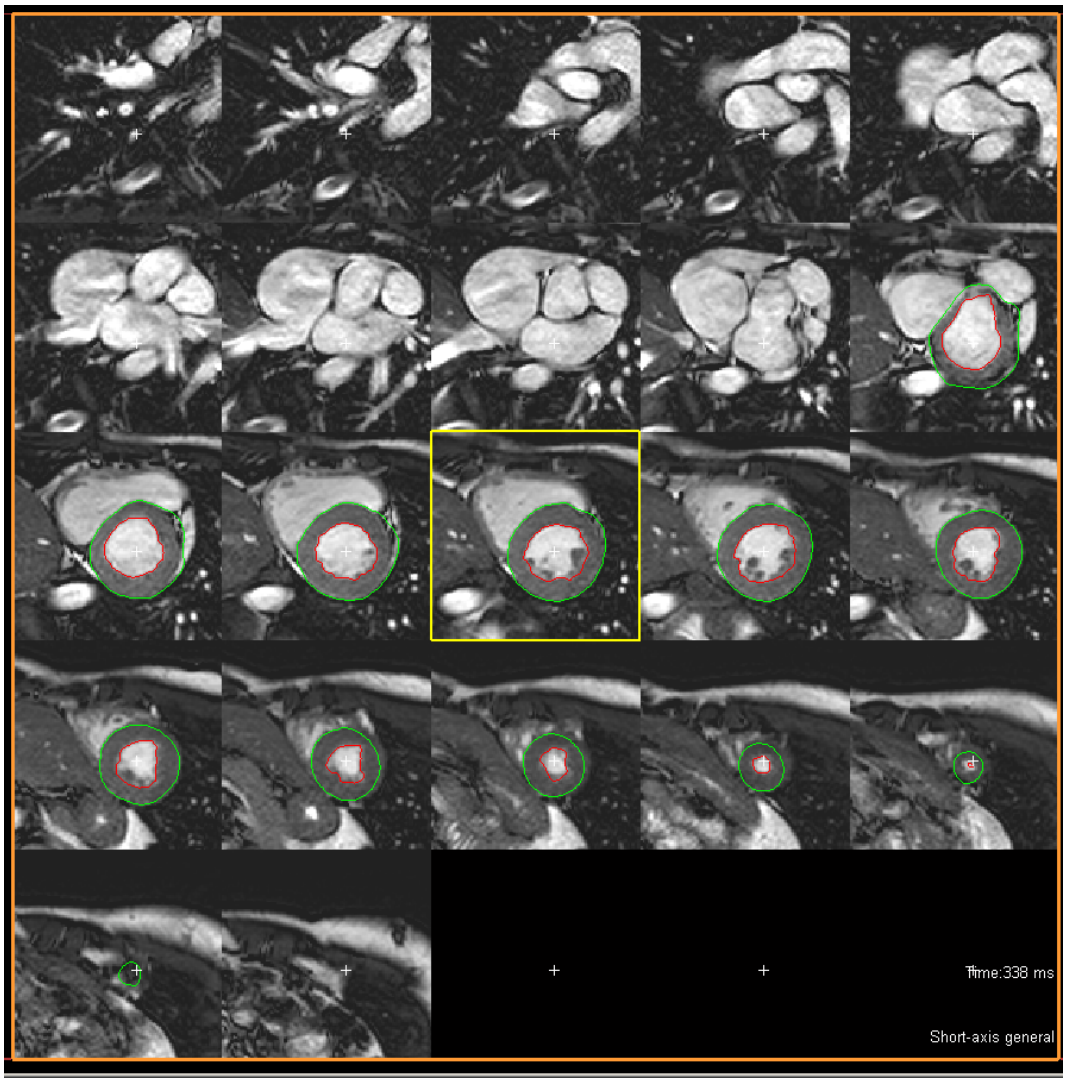



Figure 6: Screen-shot of the program showing an image stack in montage view.

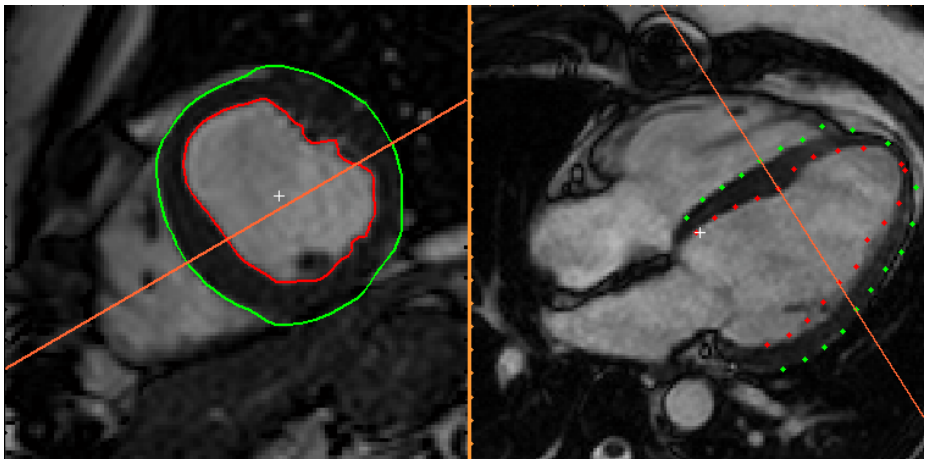


Figure 7: Contours are visible in other image stacks as dots. This is very useful to delineate structures that might be difficult to see in only one image plane.

In the image panel to the left one slice is displayed. To view a different slice use the up/down arrows on the keyboard. The right image panel a so called m-mode image is shown (the term comes from ultrasound motion-mode). This is a resampling of the left-image along the white line over time. The resampling line can be moved and angled by left-clicking on the blue circles and dragging the mouse while the left mouse button is hold down. Along the lines there are two callipers shown as a white cross. The same callipers are showed in the right image as vertical white dotted lines. Distance between the two callipers is displayed under the m-mode image. To measure time events two time bars are shown in the m-mode image. These can be dragged with the mouse, and the time between them is shown above the m-mode image.

This viewing mode can also be used to make measurements. An example on how this can be used is given in Section 11.1.2.

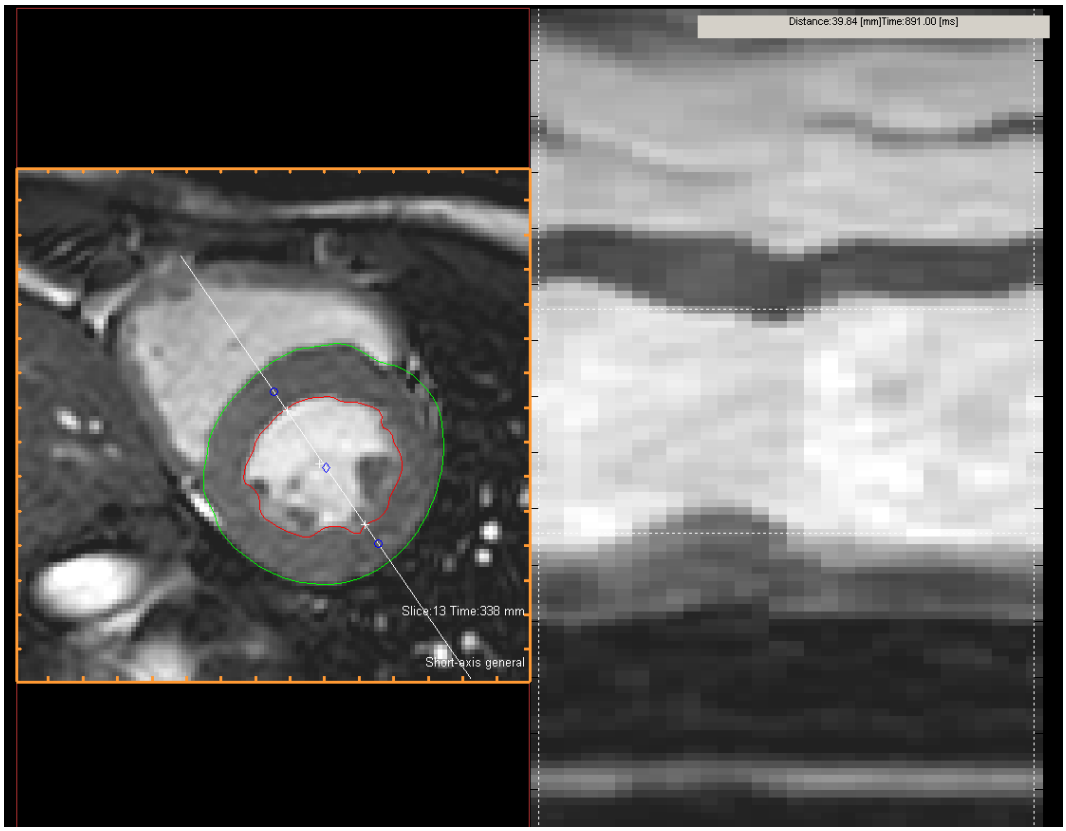



Figure 8: Screen-shot of the program showing an image stack in M-mode viewing mode.

## 10.6 Viewing velocity encoded image stacks

For velocity encoded images it is possible to view both the magnitude image and the corresponding velocity encoded image(s). In the thumbnails a white box is drawn around magnitude and phase image to indicate what image stacks belong to each other. For more details see Chapter 20, Flow Analysis.

## 10.7 Playing images as a cine-loop

In the main icon toolbar the controls what time frame of the image sequence is displayed. The icon (`Shift-left`) shows previous frame but applies to all visible image stacks. It displays the previous frame for the current image stack, and tries to find the corresponding time frame for all image stacks. The icon (`left`) displays the previous time frame for the active image stack. You can also use left arrow button. The icon plays the active image stack sequence as a cine loop. The icon (`right`) shows the next frame for the active image stack. You can also use right arrow button to show the next frame. The icon (`Shift-right`) performs the same operation as , but forward in time instead. Control and arrow keys show previous/next frame for all image stacks. The icon  increases the playback speed, and decreases the speed. Another convenient method to quickly move between time frames is by clicking in the volume graph. Here you can also interactively drag which time frame is used as end diastole (ED) or end systole (ES). You can also switch between systole and diastole by using the hot keys `d` and `s`, respectively. Yet another way to scroll between time frames is to use the mouse wheel and at the same to press `Shift`.

## 10.8 Synchronizing image stacks

It is often required to synchronize image stacks in time and slice. This can be done by using the Shift-key. Shift-left/right key shows previous/next frame and synchronizes all visible image stacks in time. For image stacks that have different number of time steps the nearest time frame is shown. `Shift-S` and `Shift-D` toggles between systole and diastole in all visible image stacks.

## 10.9 Loading and storing images

The top left section of icons contains functionality to load and save image data. The first icon opens a file loader GUI described in Chapter 9. The second icon opens the patient database described in Chapter 37. The third icon saves all the loaded image stacks to one file. The fourth icon opens a connection to a PACS server, see Chapter 39 for further details.

## 10.10 Tool palette

The tool palette is located at the lower right corner of Segment main graphical user interface. The tool palette have several modes in which different tools become available. The current mode is indicated as black text on blue background. The current active tool is indicated by displaying the tool in a darker gray color. Generally, with few exceptions all functions in the program only applies to selected slices. Selected slices are indicated with a yellow box in the montage view. The functionality of selecting slices can only be used in the montage view. An alternative to select slices is to use the short key `Ctrl-A` that selects all slices. To pan the image use the tool and move the mouse.

There are some general tools that is present in all tool modes, and these are; to undo last contour edit command, to adjust brightness and contrast (Hold down the mouse button and move left right to adjust contrast and up/down to control brightness), to select slices or image stacks. This latter tool is the default tool. Contrast and brightness can also be adjusted without first clicking the icon , by using the middle mouse button instead. There are also in some of the modes that translates ROI's and contours or the whole image if no ROI or contour was clicked, and that scale ROI's and contours.

### 10.10.1 Left ventricle tools

The left ventricle tools are shown in Figure 9. Colors are used to indicate endocardium (red) or epicardium (green).

On the first row (from left to right); is used for an interpolated contour mode to click out points to control the endocardial contour. To close the contour and interpolate a line between the points, shift click in the image.

Figure 9: Left ventricular toolpalette.

The points can interactively be dragged. The second tool is used to manually draw the endocardium. The third tool is to automatically refine the endocardium. The fourth tool puts endocardial pins that guides the automated segmentation. The fifth tool is to interactively drag the endocardium with the mouse.

On the second row is the same as the first row except that the tools applies to the epicardial contour instead of the endocardial contour.

On the third row (from left to right): The first icon automatically segments both endocardium and epicardium of the left ventricle. You need to ensure that the center '+' is in the middle of the ventricle and that all slices that covers the left ventricle are selected, see Chapter11. The second icon automatically segments the endocardium in the selected slices. The third icon automatically segments the epicardium of the selected slices. The fourth icon attempts to remove the papillary muscles. This can be use multiple times to successfully remove them. The last icon deletes the segmentation in the selected slices.

Generally, the space key can be used to toggle between the endo and epicardial tool counterparts.

### 10.10.2 Right ventricle tools

The right ventricle tool palette is shown in Figure 10. The icon is used to click out points in the interpolated contour tool for the right ventricle

endocardium, and is used for the epicardium, respectively. The icon is used to manually draw the right ventricle (RV) endocardium. The icon is used to automatically delineate the RV endocardium. Note that the RV tool is not as automated as the LV tools. The icon is used to refine the RV endocardium. The icon is used to put RV endocardial pins for guiding the automated RV segmentation. The icon is used to manually drag the RV endocardium. The icon is used to manually draw RV epicardium.

Figure 10: Right ventricular toolpalette.

### 10.10.3 Viability/Scar tools

The functions described in this section is off label use and for investigational use only.The viability tool palette is shown in Figure 11.

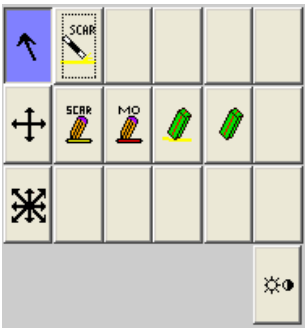



Figure 11: Viability toolpalette.

The icon is used to automatically delineate infarct region on MR delayed enhancement images. The icon is used to manually delineate infarction. The icon is used to manually delineate regions with microvascular obstruction. The icon manually removes infarction. The icon erase manual corrections of infarction. The show the manual interactions and regions of microvascular obstruction you need to press the key `o` to toggle the display.

### 10.10.4 Miscellaneous tool mode

The miscellaneous tool mode is shown in Figure 12.

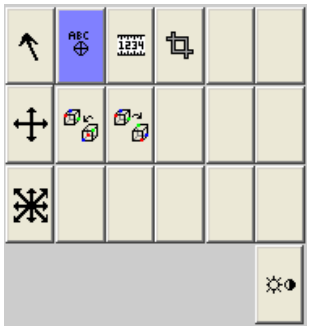


Figure 12: Miscellaneous mode toolpalette.

The icon is used to place annotation points. The icon is used to make length measurements. Left click with mouse at the starting point and hold mouse button down and move the mouse to end point. It is possible to interactively drag and refine measurements later. The icon is used to crop the current image stack. The icons and are used to rotate the image stack in 3D space.

### 10.10.5 ROI tool mode

The toolpalette for region of interest analysis (ROI) is shown in Figure 13. The first tool is used to manually delineate region of interests. The icon is used to automatically outline a vessel from scratch. Before using this place the center point (+) in the middle of the vessel. The icon refines a vessel. This is done in all time frames if the checkbox ☒ Single Frame mode is unchecked. The icon copies the ROI contour to next time frame and refines it. The icon tracks a ROI over the entire cardiac cycle. The icon

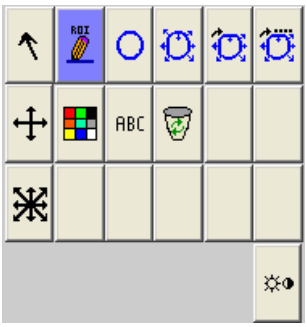



Figure 13: Region of interest mode toolpalette.

selects current color to use to draw ROI's. The icon ABC is used to name the current ROI.

## 10.11 View tool mode

This mode is useful for quickly picking different views of the image stacks. The toolpalette is shown in Figure 14.

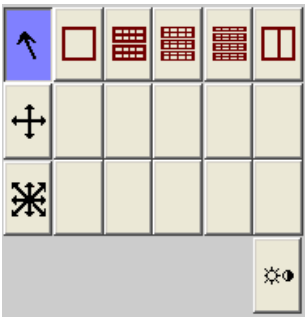


Figure 14: View mode toolpalette.

The first icon shows cine images, shows both cine images and the corresponding short axis delayed enhancement images, shows cine, delayed enhancement and perfusion images, shows a stress display, shows a flow view with a magnitude and a phase contrast image to the right. This mode is subject for future improvements.

## 10.12 General view and reporting functionality

The report tool creates a full text and graphical report of all the measurements for all image stacks. The icon starts a movie recorder that allows to store an image stack as an `.avi` movie. It is also possible to directly export a movie under the Export menu.

There are seven tools available to visualize or handle image stacks. Each of these starts separate graphical user interfaces to view and manipulate image data. They are all available as icons on the main menu. The icon starts the general segmentation tool described in Chapter 13. The icon starts a tool to do multiple planar reconstructions, described in Chapter 26. The icon starts the Image Fusion Module. The icon starts a three dimensional visualization tool, and an example of a such visualization is shown in Figure 16. The icon starts a volume rendering tool. This tool is under development and currently unavailable. The icon starts a tool to do regional wall motion per slice analysis described in Section 22.2. The icon starts a tool to do bullseye visualization of wall motion and infarct parameters. The last icon starts flow analysis tool, described in Chapter 20.

# 11 Segmentation of the Left Ventricle

Before starting to describe segmentation of the left ventricle it is of importance to define what do we consider as the left ventricle.

## 11.1 Definition of the left ventricle

At a first thought it seems very easy to define what part of the heart should be included in the left ventricle. At a second thought the definition needs to be practical and repeatable. In the program the following decisions have been made.

### 11.1.1 Papillary muscles

There are two main modes of the programs when dealing with papillary muscles. If the checkbox ☒ Exclude papillaries in the preferences are checked, then the papillary muscles are removed as much as possible (even if they are attached to the wall). This mode is **very** useful when doing wall motion analysis. However the left ventricular mass will be calculated incorrectly. To solve this problem functionality to estimate papillary muscle volume that can add the volume of the papillary muscles later. This is the recommended option. In future version of Segment a special papillary muscle ROI's will also be implemented.

In the other mode the papillaries visible in a certain slice are only regarded as myocardium if they in any part of the heart cycle collapses into the wall. This means that one papillary might be included and the other excluded as illustrated in Figure 15.

Details on how to include/exclude the papillaries are given in Section 11.3.

### 11.1.2 Mitral annulus

Long-axis motion of the left ventricle is a very important component to achieve correct ejection fractions, and volumes. The long-axis motion direction is assumed to be orthogonal to the slice direction. The long-axis

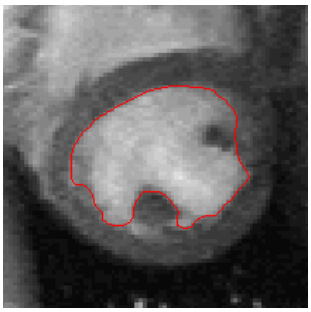


Figure 15: One papilar included and the other one excluded.

direction is shown in Figure 16.

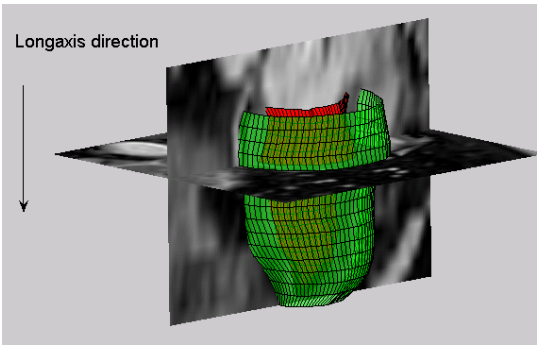



Figure 16: Three dimensional view of the left ventricle showing the long-axis direction.

Furthermore, the mitral annular motion is assumed to follow linearly with the volume curve. This assumption is used to compensate the volume for the heart long axis motion. In end diastole (defined as maximum volume) all the selected slices are used for volume calculation. In end systole (minimum volume) only a fraction of the most basal slice(s) are used for volume calculation. The amount of volume taken is proportional to the assumed long-axis motion and the left ventricular volume (without correction) at the current time frame. For instance if the assumed long-axis motion is 1.5 cm and the slice thickness is 10mm, then in end-diastole all of the volume in the basal slices are counted, but in end-systole the most basal slice is not counted at

all and the second most basal slice is counted by 50%. To see what volume is included there is a checkbox ☒ View Volume Outline on the main graphical interface.

The recommended method of finding long-axis motion is to load separately acquired long-axis images, and use the m-mode tool to measure it manually. The method to measure long-axis motion is illustrated in Figure 17. Another possibility is to let the segmentation algorithm auto detect a long-axis motion so that the variation of the left ventricular mass is minimized. This option works in certain cases and fails in other. A third possibility is to manually adjust the long-axis motion and see at what long-axis motion the segmentation 'fits' so that only left ventricular myocardium is included in the basal slices.

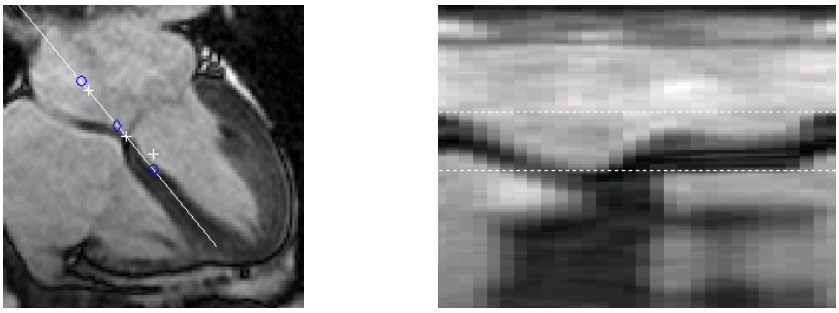


Figure 17: Measurement of long axis motion. Left panel shows placement of M-mode line. Right panel shows M-mode image with placed measurement calipers (dashed white line).

## 11.2 Start the segmentation process

In order to start the segmentation process you need to selected the slices that should be included in the segmentation. Slices are selected by left mouse click on the desired slice and drag the mouse while the left button is hold down. Since the long-axis motion is around 1-2 cm (in healthy normals) the most basal slice is contains parts of the left atrium in end-systole. Often it is good to play a loop while selecting the slices.

Make sure that the basal-apex orientation is correct. The most basal slice should be in the upper left corner. If not then select Image Tools→Flip z and x described in detail in Chapter 15.

To do a fully automated segmentation select slices so that the most apical slice contains no endocardium, and only epicardium. The basal limit should be the most basal slice that have left ventricular myocardium at least in some part of the heart cycle. Make sure that you selected the correct image type when loading the image stack (MR SSFP, CT...). This can also be set afterwards by right-clicking on the image stack thumbnail image. Make sure that ☒ Single Frame Mode checkbox is unchecked, and that ☒ Exclude papillaries in the preferences is checked. Then press the to start the segmentation.

Manually adjust the segmentation results if necessary, see Section 11.3 for details.

When pleased with both endocardial and epicardial segmentation adjust long-axis motion slider according to measured long-axis motion or a manually selected value that fits with image data (use view volume outline) or use the automated detection of long axis motion. Select Segmentation→Estimate papillary volume.

## 11.3 Edit the segmentation result

Unfortunately the segmentation result is not always as one would desire. We have done as much as we possible can to implement and design a segmentation algorithm that is robust and accurate, but despite that the algorithm do fail in certain cases, and especially on the epicardial contour.

There are many implemented methods to manually edit the segmentation result. Different methods are good in different situations. I recommend to learn them all, and by experience learn in what situations the different types of manual interaction works best. If you experience that editing is a cumbersome task, then you are probably doing it the wrong way.

When the segmentation fails completely, please check the following items:

- Double check that you selected the correct Image type (MR Gradient

echo, MR SSFP, CT contrast etc) when you loaded the data. This is very important for the segmentation result. Select Edit→Set image type from the main menu to do this, or right click on the thumbnail.

- Double check that a good center point is chosen. In some cases where the heart is not cut in a true short axis plane, then the same center point cannot be used for all slices. You will then have to do the ventricle in two half's, and adjust center point. Changing the center point (white +) is done by dragging the center point with the mouse.
- Try also to not include the most apical/basal slices, and use the up/down propagation tools that are available.
- When the epicardium fails, ensure that the endocardial segmentation is satisfactory before starting to delineate the epicardium. If you have used the fully automatic segmentation mode and was forced to do large adjustments on the endocardium, then select the mid ventricular slices and press to re-segment the epicardium. For the most basal slices select each slice and press usually gives a more satisfactory result.

There are several methods to manipulate the segmentation result. Each method have different applications where they work better, and it is a learning process to learn which tool to use in different situation.

### 11.3.1 Undo segmentation

To undo the latest segmentation operation select undo from the tools menu, or using the undo icon , or using the hot key `Ctrl-Z`.

### 11.3.2 Redo segmentation

If the segmentation failed for one, or a few slices, then one of the easiest ways to simply select these slices and do the segmentation again only for the erroneous slices. The difference with this second run compared to the segmentation of the complete ventricle is that the segmentation algorithm only looks at the intensity distribution in the selected slices when trying to estimate blood pool intensity.

### 11.3.3 Copy segmentation (propagate)

A very efficient way of handling erroneous slice is to copy a the segmentation results from an adjacent slice. This is especially efficient in the more

basal slices. The program copies the slices and refines the position of the contours by a few iterations. To propagate a segmentation forward in time one time frame, press Ctrl-F. If the endocardial pen is selected then the endocardium is propagated, and if the epicardial pen is selected , then the epicardium is propagated. The hot key Ctrl-F also applies to ROI's if the ROI pen is selected.

### 11.3.4 Estimate apex

The image quality in the apical region is in some imaging modalities very poor. Therefore a function to estimate apical region is implemented, and is found in the Segmentation→LV tools menu. The function copies the most apical slice downward, decrease it slice and refines the contour with a few number of iterations. This process can be iterated if several apical slices needs to be estimated. It might be advantageous to combine the Estimate apex function with the refine functionality.

### 11.3.5 Estimate apex only epicardium

Same as estimate apex only that this function does not copy the endocardium, useful for the very most apical slice where the blood pool is not visible.

### 11.3.6 Place pins

Pins are objects places in space and time, that attracts the contour. There are endocardial and epicardial pins, and they attract respective contour. To start placing pins select one of the two icons by the following icons , and to put a endo- or epicardial pin, respectively.

Subsequently after selecting these icons, each click in the image puts a pin. To stop placing pins select the slice selector tool icon . The pins can be removed by right clicking the pin and select Remove this pin. To erase all pins in the entire image volume, or the current slice, right click in any place of the image (where there are no pins) and select remove all pins from the popup menu.

Each time a pin is placed the contour is refined by a few iterations. Often more iterations are required to achieved the desired shape. To do so click on the refine tool (see under Section 11.3.11). Sometimes it is hard to really get the program to go to the desired pins, it can then help to put some pins,

and completely redo the segmentation in that slice. When redoing the segmentation with some pins selected it is important to have the pins roughly symmetrically placed. For instance the left placement in Figure 18 will not work, but the right placement will.

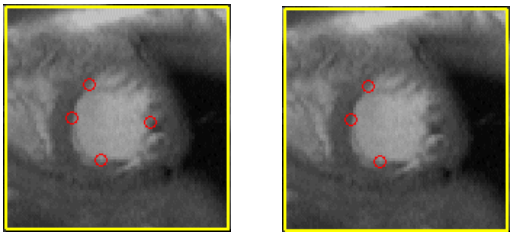


Figure 18: Asymmetric and symmetric pin placement.

Often a better alternative than placing pins is to manually draw a part of the contour.

### 11.3.7 Manually dragging the contour

For small adjustments it is possible to manually drag the contour by first selecting the drag-tools on the toolbar ( and for endocardium and epicardium, respectively). Then select the desired contour by pressing the left mouse button and hold it down. The segmentation algorithm is the running in realtime while the mouse is dragged, but the segmentation algorithm works only for the current slice.

### 11.3.8 Manually draw a section

This functionality is chosen by the two icons ENDO and EPI for endocardium and epicardium, respectively. If you do draw the complete contour then the actual drawn contour is taken. If there were no segmentation in that slice, then the segmentation is copied to all time frames. A quick method to toggle between drawing epicardium, and endocardium is to use the space button on the keyboard. On the preferences menu there is an option to whether you want to place pins along the drawn contour. If you are doing time resolved segmentation, then it is recommended is to set this to on, and after drawing a part of the contour select refine to 'propagate' the change to adjacent time frames. Manually drawing a part of the segmentation is probably the easiest

way to make changes in the segmentation if you only need end diastole and end systolic segmentations.

### 11.3.9 Removing papillary muscles

One approach to remove papillary muscles is to fit the segmented contour with an 'buckled' ellipse, and thereafter refine the segmentation a few iterations. This option is automatically done if the option ☒ Exclude papillaries in the preferences is toggled. This functionality is especially useful in conjunction with the track tool described above. Sometimes it is often advantageous to use this functionality twice. An example is when the ☒ Exclude papillaries have failed to remove the papillary muscles in some slices. Select these slices, and press `Ctrl-V` (remove papillary muscles) or tool , and `Ctrl-R` (refine endocardium). If it fails then try it once more, if it fails again then resort to drawing parts of the endocardium.

### 11.3.10 Track tool

In some cases one want to exclude the papillary muscles, then one can try the Track-tool functionality. Select the desired slices, and press the hot key `Ctrl-T` or Track-tool in the Segmentation menu. The track tools tries to track the contour of the endocardium in each selected slice, and time frame. One disadvantage is that it does not include time in the calculations, and therefore the result might be a bit discontinues in time. A remedy for this is do a refine (best if all slices are included) after the track-tool is run.

### 11.3.11 Refine segmentation

Refine runs the segmentation algorithm a few iterations, and thus further refines the segmentation. Note that the optimization is only run for the selected slices.

### 11.3.12 Translating the segmentation

The segmentation can be translated/dragged in each slice. This is done by using the icon in the toolbar palette. Note that the usage of this translation is especially useful in conjunction with the import segmentation option in the main menu. Then a segmentation from one imaging technology can be overlaid an image of a different image stack if they were acquired using

the same coordinate system. A practical application is doing the segmentation on cine gradient echo or cine SSFP images and overlay that result over late enhancement images. Under the segmentation menu it is possible to translate/move selected slices towards the base/apex.

### 11.3.13 Scale the segmentation

In some slices, and typically the apical slices scaling the segmentation can be very effective correction. Scaling can be done with the ✳ tool. Scaling can often successfully be combined with the refine operation.

### 11.3.14 Removing segmentation result

The segmentation result can be removed with the right mouse click pop-up menu (shown in the place pin section above). These function are also available in the main menu under Segmention. A quick method to erase segmentation in selected slices are to use the delete key on the keyboard to remove segmentation from selected slices. Note that if the radio button ☒ Single frame mode is selected, then the segmentation in the current time frame is deleted, otherwise, the segmentation for all time frames in that slice are deleted.

# 12 Segmentation of the Right Ventricle

The right ventricle is much more geometrically complex than the left ventricle. The walls are much thinner and there are more and complex trabeculation. This is one explanation that there are currently in Segment no really good automated tools to do segmentation of the right ventricle. This will be improved in future versions of Segment.

Currently what is available are the same basic functionality as for the left ventricle. For the mid ventricular slices the automated methods (manual draw+refine can be used).

At the current stage we do not recommend to do time resolved segmentation of the right ventricle since the drawing and edit tools are so poor. We would the suggest to remove all RV segmentation except systole and diastole. An example of segmentation of the right ventricle is shown in Figure 19.

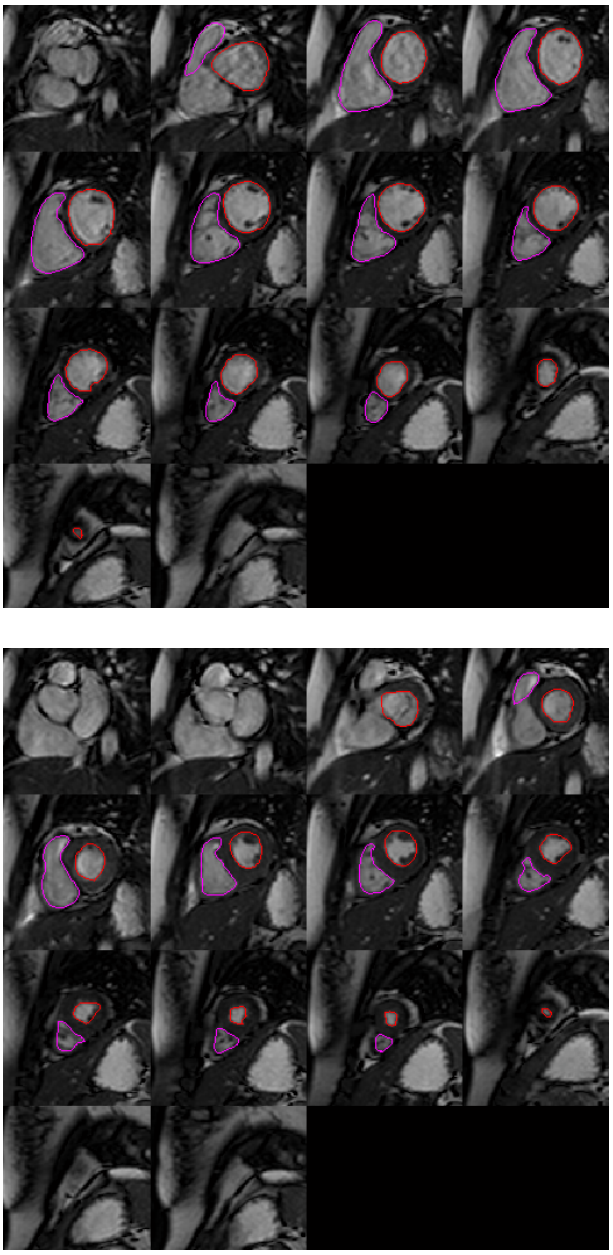


Figure 19: Top: Segmentation of the right ventricle in diastole in a short axis image stack. Bottom: Segmentation of the right ventricle in systole in the same short axis stack. Note the relative large long axis motion.

# 13 Segmentation of General Objects

The functions described in this chapter is off label use and for investigational use only. This module is useful for delineating complicated 3D anatomical objects. Since it is less specialized than the segmentation of the left ventricle, it is less automated.

The functions described in this chapter is off label use and for investigational use only.

Promising new techniques such as prototype based image segmentation [1] has been incorporated in this module, Section 13.8.

## 13.1 Viewing data

The graphical user interface is shown in Figure 20. There are three orthogonal views and one view of the speed image further described in Section 13.2.2. The slice position of the upper right image is shown as a red line in the two other slices. The leftmost lower image, and rightmost lower image are shown as green, and blue lines, respectively. When the selection tool is active then by left click in any of the three orthogonal views the postion of the image planes can be adjusted. There are four checkboxes that control how the data is displayed. When the checkbox ☒ as MIP is checked then the shown image is a MIP image (Maximum Intensity Projection). Note that contour overlay is not done in the MIP projection. The checkbox ☒ Interaction shows manual edits and region growing interactions. Placed seed points and added areas are shown in green and removed areas are shown in blue. The checkbox ☒ Selection shows the segmented object in red color. Finally, the checkbox ☒ Outline determines whether the object outline (displayed in yellow color) is shown or not.

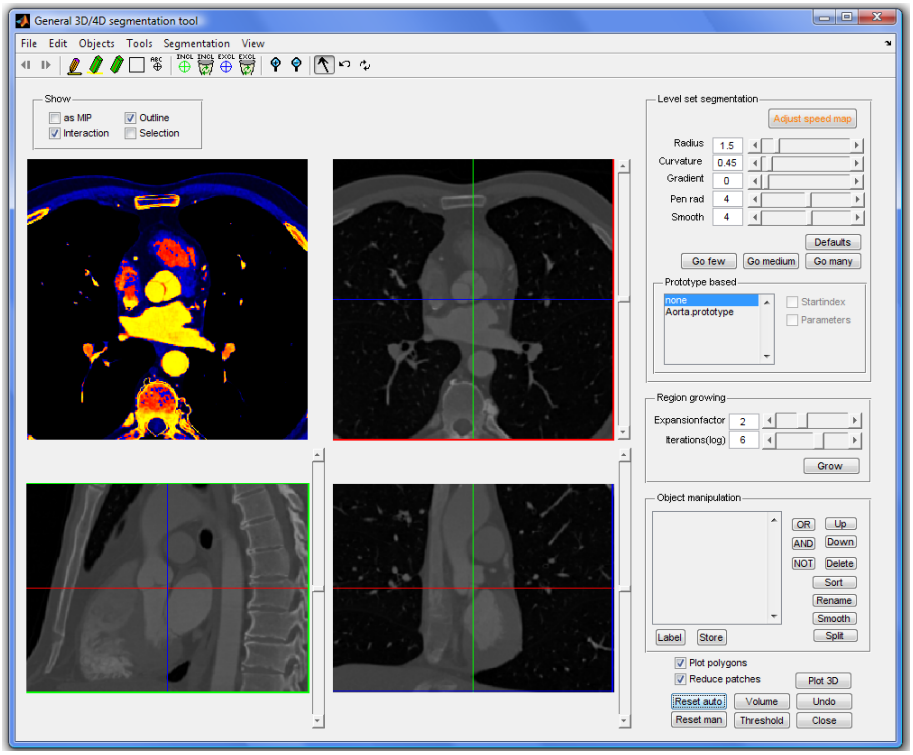



Figure 20: Graphical user interface for general object segmentation.

## 13.2 Level set segmentation

### 13.2.1 Algorithm

The algorithm is based on a very fast level set algorithm [2]. From a seed point or set of seed points the object is expanded outwards. The expansion is stopped at edges or regions with low signal intensities. The expansion is also penalized for large curvature, i.e. the algorithm favours object with low local curvature. The expansion (or contraction) is allowed to continue for a number of iterations. The key to the sucess of the algorithm lies in adjusting an appropriate expansion speed.

### 13.2.2 Optimizing expansion speed

Before adjusting the expansion speed you should draw some seed points. Image intensity for the seed points are used in the calculation of the expansion speed image, for details, see below. There is a separate graphical user interface to help adjusting the speed image calculation. This user interface is shown in Figure 21. In the upper left panel, an intensity histogram of the complete volume is shown. In the lower left panel a function that maps signal intensity to local expansion speed is shown. In the upper right image panel a magnitude slice is shown. Different slices can be selected by usage of the Slice slider. In the lower right image panel the corresponding speed image is shown. Bright red and yellow colors denote expansion, whereas dark and blue colors denote contraction. Four different speed mapping modes can be chosen; Gaussian, Positive slope, Negative slope and Prototype shaped. The Gaussian shape is useful when one want to delineate objects within a certain signal intensity range. One example is mapping certain Hounsfield units from CT images. In future versions of `Segment` it will be possible to store a set of speed mappings, and couple them to the normalized image values used in `Segment`. The Positive slope is useful to segment regions that are brighter than a certain image intensity, and the Negative slope is useful to segment regions that are darker than a certain image intensity. The Prototype shaped speed mapping mode is further described in Section 13.8. The mapping is 'translated' by adjusting the Offset slider. The default behavior is that the mean signal intensity is used as 'zero' level of the speed intensity mapping. This is useful since after selecting seed points only small adjustments of the Offset slider is the usually required. By unchecking the checkbox Intensity from seed as offset the 'zero' level will instead be 0.5. The slope of the map-

ping is adjusted by usage of the Width slider. When pleased with the settings on how the speed image is calculated press Dismiss.

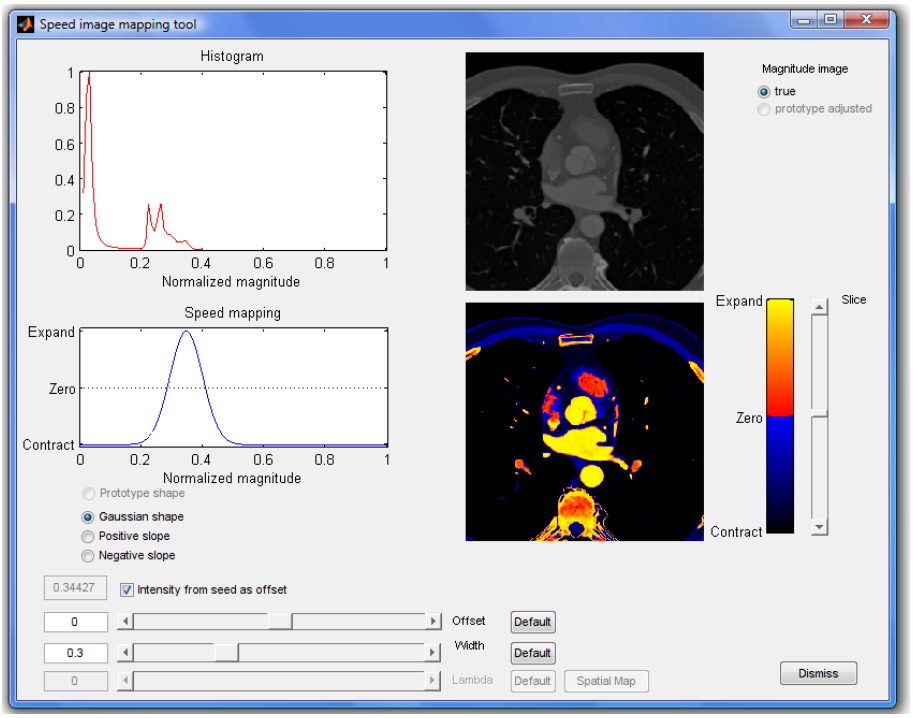



Figure 21: Graphical user interface to adjust speed image.

### 13.2.3 Start the segmentation tool

Start the segmentation process by first draw some seed points/regions by selecting the draw tool . The thickness of the pen can be adjusted by the slider pen radius. The pen draws a sphere of the radius set by the slider in all three or four dimensions, so you need to start to think and work three dimensionally. If the checkbox ☒ Manual interaction is checked then added regions with  is colored in green and removed regions with the tool  are colored blue. By using the tool  it is possible to remove user interactions created with the two tools  and , respectively.

After drawing some seed points adjust the speed image such as the desired object(s) is shown in a red or bright yellow color. This is described in detail in Section 13.2.2 above. The user interface is started by the Adjust speed map. This adjustment is rather critical for the final result, so do this step with care.

Start the segmentation algorithm by the pushbutton Go few (iterations). The smoothness of the final segmentation result can be adjusted by changing the algorithms penalty for curvature. This is done by the Curvature slider. Note that you can also smooth the segmentation result. This is described in detail in Section 13.6. The slider Radius control how large volume is used for curvature calculation. The slider Gradient control how sensitive to boundaries in the image the algorithm will be. Large value means the algorithm is more likely to stop expanding at boundaries. If thecontour of the object expands as planned then continue with Go medium or Go many if necessary.

## 13.3 Manual interaction

You can manually edit the result by using the drawing tool or the removal tool . For each voxel in the image volume manual corrections can be of three kinds; no change, i.e. no manual correction, or pixel included, or pixel removed. By using the tool ☐ it is possible to draw a box in any of the three orthogonal views. This box can then be filled so that it is avoided in the delineation or included in the delineation. This is very useful when one want to manually exclude large portions of the image stack from the segmentation. Interactions to edit the segmentation can also be done with region growing.

## 13.4 Region growing

Region growing is a tool for doing a new segmentation and/or automatically interact with existing segmentation by only placing one inclusion and/or exclusion point. The result from the segmentation is shown in the same way as the manual interaction and can therefore remove and add to an exisiting segmentation. If no segmentation exists this tool creates a new segmentation.

### 13.4.1 Algorithm

The algorithm is based on a level set segmentation but the expansion speed is automatically calculated from the inclusion and/or exclusion point and only one inclusion and/or exclusion object can be segmented at a time.

### 13.4.2 Start the segmentation tool

The segmentation is started by placing an inclusion and/or exclusion point in the image. This is done with the tools and/or . The inclusion point should be used when a new segmentation or addition to an exisitng segmentation is the desired result. The exclusion point should be used when a part of an object shall be removed from an already exisiting segmentation. It is also advantageous to place both an inclusion and exclusion point in the image when a new segmentation is the desired result since it can give a better estimation of what intensities to include in and exclude from the segmentation. When the inclusion and/or exclusion point is placed in the image press the button Grow. To set a new inclusion and/or exclusion point use the tool once more and the old point will be removed. It is also possible to remove the inclusion and/or exclusion point with the function and/or . If more iterations is desired use the iterations slider or push the grow button once more. If more intensity expansion is desired use the expansion slider to increase or decrease it. The expansion speed can be seen in the speed image view after pressing grow.

## 13.5 Object manipulation

When you are pleased with an object or part of an object you can store that to a quick pick-list by the pushbutton Store. With multiple stored objects you can perform binary operations on them to merge or combine objects in other ways by using the OR, AND, NOT. You can also rename objects by the using the pushbutton Rename, or sort them in the list by the buttons Up or Down. The pushbutton Sort sorts the object by decreasing volume.

If you have many objects it is possible to store them all under different names. This is done by the function Label. This label function can also be useful to detect if two objects are joined or not. The used connectivity is

6-connectivety.

If you have one object that you want to try to split into two objects, this can be done by choosing the object in the list and using the function Split. The function erodes the object to split it at its weakest point. After the object is split into two or more parts, the algorithm reconstucts the parts so that the effects of the erosion are removed. The new objects are stored into the list.

## 13.6 Smoothing objects

The object is internally stored by allocating one byte per voxel. If this byte contains a value over 128, then the voxel is inside the object, otherwise the voxel is outside the object. The algorithm is binary by construction, and each voxel is given either the value 255 or 0. The contour of the exported files are created by the marching cubes algorithm, and to create a smoother result smoothing of the object representation can be performed. The slider Smooth controls the radius of a smoothing filter. The value is the number of mm to the 30% signal intensity drop of the filter. You need to experiment with the filter setting to achieve proper smoothing. For undo history and storing objects only a binary representation is used, due to memory considerations. In the Segmentation menu there is an option to create a plot of the smoothing filter.

## 13.7 Viewing final result

By pressing the pushbutton Plot 3D the 3D image is plotted in a separate window that can be easily rotated and zoomed. There are two checkboxes that controls the view of the isosurface ☒ Plot polygons determines whether polygons are plotted or not, ☒ Reduce patch determines whether the number of polygons should be removed by 80%.

## 13.8 Prototype based segmentation

The prototype based segmentation is a newly developed algortihm for introducing a priori information for a specific application to the level set method

used in this tool. The prototype holds both spatial information to constrain the segmentation, seed points for initialisation of the segmentation and a speed mapping function. By the use of a prototype the general segmentation can be made nearly automatic. The main idea behind the algorithm is to rather model a constrain of the segmentation, stored as a spatial map, than to model the object to be segmented. For more detailes on the algorithm see [1].

A prototype can be generated for a specific application by Medviso AB please contact us at `info@medviso.com` to discuss your desired segmentation applications.

To start the prototype based segmentation a couple of landmarks, defined in the protoype, need to be set by the use of the point tool . The landmarks can be set in any of the orthogonal view panels. The points shall also be named according to the information in the prototype. The specific prototype is chosen in the listbox in the panel Prototype. After the selection has been made calculations is done to align the prototype to the landmarks. When the calculations are done a light green outline is shown in the orthogonal view panels indicating the startindex of the segmentation which is used as seed points. Also the parameters radius, curvature and gradient has been set to an optimal value which was stored in the prototype. It is possible to not use the predefined startindex and/or parameters by unselecting the checkboxes ☒ startindex and ☒ parameters in the Prototype panel.

To adjust the speed image push the button Adjust speed map. The speed image for prototype based segmentation differs in several ways from the usual levelset segmentation. The image is automatically intensity adjusted which can be seen by the magnitude image being Prototype adjusted.The histogram is calculated from the adjusted magnitude image. The speed mapping mode is Prototype shaped, and the shown function is a probabilistic fucntion stored in the prototype. Finally the Lambda slider and edit are enabled, this controls the influence of the spatial map. The spatial map is an a priori mapping stored in the prototype which constrains the segmentation. The default value of the parameter lambda is also stored in the prototype. The speed image shown is calculated from the speed mapping and by subtracting the spatial map. If any adjustments need to be done it is possible to change the Offset and Zero level but firstly try to adjust the factor Lambda since the most important part of the prototype based segmentation is the spatial map.

When pressing the button Spatial map the spatial map is shown in a separate window. When satisfied with the speed image, press Dismiss. To do the segmentation press either Go few, Go medium or Go many. If more iterations is desired it is possible to choose if the startindex from the prototype should be used as startindex should be used or not in the checkbox ☒ Startindex.

# 14 Save and Load Segmentation

A key feature in Segment is that all measurements and user interaction can be saved so that is possible to go back and see how the analysis was done.

Saving and loading works differently in the Clinical mode or in the research mode. In the clinical mode then Ctrl-S automatically saves to the patient database, and in the research mode you will be prompted where to store the file. Loading operations in the clinical mode opens the patient database, whereas in the research mode it opens the file loader GUI.

## 14.1 Save images

Segment is able to save files in three diffrent formats. One old and soon to be obsoleted that stores only the image information of one single image stack, one that stores all image stack with all segmentation into one single file and one that stores all images stacks with all segmentation into one single file that is also a valid DICOM file. The second format is the most stable and is recommended when one observer is reviewing the images, and one would like to have the opportunity to go back and check how the analysis where made. If one needs to store the file in an enviroment which only accepts DICOM images, such as a PACS, one can use the third format.

### 14.1.1 Save both image stacks and segmentation to one file

This function saves both the image stacks and the segmentation to one file. This is the recommended way to save the images.

### 14.1.2 Save both image stacks and segmentation as

Same as above, but asks for a filename.

### 14.1.3 Save only segmentation

To save the segmentation results (including the measurements of mass, distance measurements, viability, and volumes etc), select the function Save Segmentation under the File menu (hot key is `Ctrl-S`). Then the program asks for a filename. The file extension should always be set to `*.seg`. Note

that the segmentation file also contains scar delineations, roi's for flow analysis etc. When comparing segmentation results for different observers it is usually better to store them as separate image files with segmentation. Note this function only saves the segmentation, **not** the images. This function is kept for backwards compability and may be dropped in future versions of Segment.

### 14.1.4 Save as DICOM

To save as DICOM file select Special save in the File menu. Then select Save as Dicom. You will be prompted for location and filename.

## 14.2 Load segmentation

To load a segmentation select Load Segmentation under the File menu. The current limitations of this operation is that you should not have removed / reordered any slices compared to when you saved the file. This limitation might be removed in the future. When loading some elementary error checking is done to ensure that the loaded segmentation indeed was done on the same image stack. To disregard this safety check see importing segmentation, below.

## 14.3 Importing segmentation result

The difference between loading and importing segmentation is that the error checking is disabled. This means that it is possible to load a segmentation from another dataset, and overlay that on the current image stack. This could be especially useful for instance with late enhancement image where the delineation can be performed on gradient echo and SSFP cine images, and then be overlaid on a late enhancement images. See Section 11.3 on details how to translate the segmentation loaded segmentation.

## 14.4 Hints

Setting the data path and export path in the preferences menu (see Chapter 25) saves a lot of work when frequently loading or saving images. When performing studies where the observer should be blinded to the identity of the patient, you can use the option to hide patient ID when loading the images. For more details see under Chapter 25.

# 15 Image Tools

The functions described in this chapter is off label use and for investigational use only.

There are numerous possibilities to manipulate image stacks. This chapter describes the tools found under the Image tools menu in the main menu. Many of these operations are not undoable. One workaround is to before applying the intended tool, right click on the image stack thumbnail and select duplicate image stack. By doing so you do not need to reload the image stack at least.

## 15.1 Crop image stack

This functionality is useful to crop the images to reduce memory requirement. This functionality is not available under the image tools menu, but as a tool in the tool palette . Note that this function is not undoable.

## 15.2 Remove time frames

There are several suboptions to select exactly which time frames you wish to delete. Note that when you have removed time frames, you should also save the image volume since it is not possible to directly load the segmentation if it is stored as a separate `.seg` file. Note that this function is not undoable.

## 15.3 Remove slices

It is possible to remove all selected slices or all slices except the selected slices. When removing slices, note that you may not be able to import a segmentation to the current image stack since the number of slices will not match. When removing slices and you want to use the data set later be sure to save the image stack. Note that this function is not undoable.

## 15.4 Fake in extra apical or basal slice

In some instances the most basal or the apical slice may be missing due to improper scan planning. This should be avoided and be reported back to the scanning operator. However, if it still occurs the image set might be possible to rescue the image stack with this operation. It inserts a copy of the basal or apical slice and the segmentation. The reason that this might work is that it might be possible to copy the delineation of the basal slice in end diastole to the second most basal slice in end systole.

## 15.5 Manipulate light/contrast

Once loading image data from DICOM files Segment internally converts the image data to the range [0..1]. The conversion factors are stored and the original pixel intensities can thus always be recovered.

### 15.5.1 Permanently apply light setting

When adjusting contrast and brightness the changes only affect the on screen appearance. With this option the current light setting is permanently applied to the image stack. This will then have impact on subsequent image quantification. Note that this functionality is not undoable.

### 15.5.2 Normalize image data

When loading image stacks from `.mat` files this check is not performed. Normalize image data will do this process. This process is currently not undoable even though all the required data is stored.

### 15.5.3 Invert colors

Invert colors remaps all pixels with the equation $s_{new} = 1 - s_{old}$, where $s$ denotes pixel intensity. This functionality is undoable by repeating the operation.

### 15.5.4 Precompensation

This functionality might be useful for gradient echo MR images to minimize inflow artefacts. This option scales each time frame such as the mean image intensity is constant over time. Note that this function is not undoable.

### 15.5.5 View intensity mapping

Brightness and contrast settings are implemented so that the pixel intensity is remaped before being rendered. Currently this remaping function is a cropped linear function, but will be extended to a sigmoid function in future versions of Segment. This functionality plots the current intensity mapping.

### 15.5.6 View true image intensity

The function displays the current slice and time frame, and a color scale coupled to the original pixel values in the DICOM file.

## 15.6 Set colormap for current image stack

This function sets the used colormap for the selected image stack. Supported colormaps are shown in Figure 22.

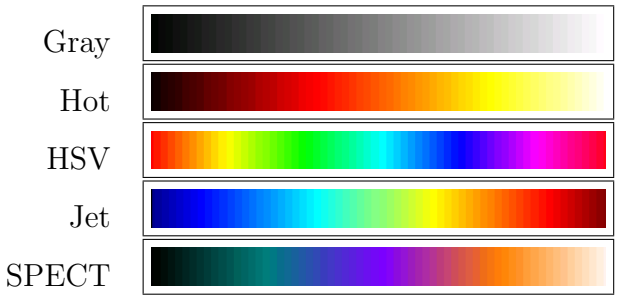



Figure 22: Colormaps.

## 15.7 Flip/Rotate image stack

By using this function it is possible to swap the direction of one axis. For instance if want to flip an image stack upside-down (apex/base) use Flip z. Flip x corresponds to what one usually would call y-axis, and for a short axis image stack this would usually be frontal/dorsal, and Flip y corresponds to left/right. Note that to preserve a right hand coordinate system it is not possible to flip in one image direction alone. Therefore, a flip in x directions also flips in the z direction. The simple flip's above is possible to do when there

is an existing segmentation. If you require to make rotations (flip between two axis) you must not have an existing segmentation. Flip x&y transposes the image, Flip x&z switch between basal/apical to up/down direction, and Flip z&t change between time frames and slices. The later option is very useful when loading non standard images. This option does not update coordinate axes so this might be dangerous to use if combining with non flipped image stacks. If you need to rotate image volume and maintain correct voxel dimensions, please use the multiplanar reconstruction (MPR) functionality described in Chapter 26. Note that currently the option to rotate 90 degrees right is not working properly.

## 15.8 Resample image stack

There are different methods to resample the original image stack.

### 15.8.1 Reformat multiplanar reconstruction)

This option invokes the multiple planar reconstruction tool described in Chapter 26.

### 15.8.2 Upsample/downsample image

By using this option it is possible to upsample or downsample the image stack. Note that resampling is only done in the in-plane direction. When downsample an appropriate anti-alias filter is applied. The used interpolation algorithm is bilinear interpolation. This functionality is not undoable.

### 15.8.3 Upsample/downsample slices

The number of slices can be upsample of downsampled. This functionality is not undoable.

## 15.9 Add noise

By using this functionality it is possible to add noise Gaussian white noise to the current image stack. The amount of noise is regulated by the std of the noise.

## 15.10 Calculate temporal mean image

This function creates a new image stack that is the temporal mean of the current image stack.

## 15.11 Set current frame as first frame

This function shifts the time series (cyclic shift) such as the current time frame becomes the first time frame in the time series. Note that it only applies to selected slices.

## 15.12 View K-space

This menu option shows the k-space for the current frame and slice.

## 15.13 Set image description

By using this menu option the image type, image view plane and imaging technique is displayed and a menu is shown where new image descriptions can be selected. Image type and image view plane is used by Segment to find what image stacks to take measurements from. This applies to the utility to summarize multiple `.mat` files and the report sheet generator. Imaging technique is used to find segmentation parameters and are therefore critical for a good automated segmentation. For further details, see Section 11.3.

## 15.14 View Image details

This function copies the most important image details to the clipboard. It is the same as the icon .

## 15.15 View and adjust image details

By using this menu option it is possible to adjust image details. Parameters that can be adjusted are Slice thickness, Slice gap, Resolution in x direction, Resolution in y direction, and time increment.

## 15.16 View and adjust patient details

This menu option starts a graphical user interface where it is possibly to view/adjust: Patient Name, ID, birth date, acquisition date, age, length, weight, sex, heart rate. The pushputton Apply to all applies the changes to all image stacks that are loaded to memory. By entering length and weight BSA is automatically calculated.

## 15.17 Remove subject identity

By using this menu option all patient data are removed from all image stacks. This is useful when sending data to a different center or for bug report purposes. This function is not undoable. Removed items are patient name, id, birth date, acquisition date, filename, and original filename.

## 15.18 Calculating image histogram

Image histogram can be calculated by using tools found under the ROI-menu. For further details, see Section 16.6.

# 16 Region of Interest Analysis

The region of interest (ROI) functionality can be used for a wide range of possibilities. To select the ROI mode you can use the hot key `Shift-F`.

You can label and color each ROI individually. For flow measurements each ROI can also be assigned with a sign that will be multiplied with the velocities inside the ROI. The default sign is positive. The following names of ROI's are reserved for various purposes:

- Remote ROI (used to implement 2SD from remote as described by [3]).
- Scar region ROI (used to implement 2SD from remote as described by [3]).
- Static tissue (used for concomitant field correction, described in Chapter 20).
- Aortic ascending flow
- Aortic descending flow
- Pulmonary artery
- Vena cava inf
- Vena cava sup
- Vena pulmonalis inf
- Vena pulmonalis sup
- Vena pulmonalis dex
- Vena pulmonalis sin
- Sinus coronarius
- Lung
- Heart

## 16.1 Creating ROI's

There are several possibilities to add ROI's. Perhaps the most intuitive method is to draw the ROI by using the . The ROI will be given the same

name, and color as the latest modified/drawn ROI. This is very useful if you would like to draw several ROI's of the same kind. Start by drawing the first ROI, name and color it. Thereafter you can continue to draw the remaining ROI's.

It is also possible to add fix sized ROI's by using the Add fix size ROI under the ROI menu. This will add a fix size ROI and you will be prompted to enter the diameter. This function applies to the current slice. Another approach is to add ROI's in the myocardium between the endocardium and epicardium. This is done by using the function Add ROI's in sector (selected slices). You will be prompted for center angle, width in degrees, percent from the wall. Zero center angle corresponds to three o clock and counting counter clock-wise. This function only adds sectors in selected slices. An example of automatic ROI placement is shown in Figure 23.

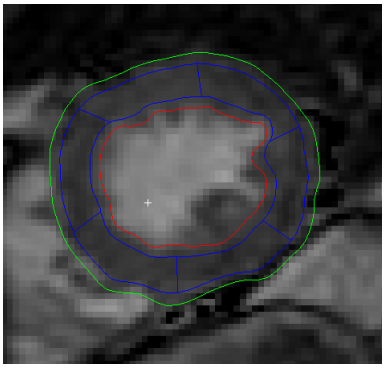


Figure 23: Automatic placement of ROI's inside the myocardium.

Another possibility to create ROI's is to convert the endocardial, epicardial or scar surface to a ROI. This is done by the option Copy endocardium to a ROI, Copy epicardium to a ROI or copy scar to a ROI. This only includes the selected slices.

## 16.2 Modifying and deleting ROI's

By right clicking on a ROI a pop-up menu appears where it is possible to:

- Delete ROI
- Set ROI label (change the name/function of the ROI).
- Set ROI color (change the color of the ROI).
- Copy ROI upwards
- Copy ROI downwards
- Copy ROI outline to all timeframes
- Refine ROI (for flow purposes, see Chapter 20).
- Switch ROI sign (useful for flow analysis).

## 16.3 Translating and scaling ROI's

ROI's are translated with the icon and scaled with . Point on ROI contour and drag while mouse button kept down to adjust to correct position/size.

## 16.4 Deleting ROI's

Under the ROI menu it is also possible to Delete ROI, Delete ROI's Using Template, and Clear All ROI's. The first menu option deletes the current (last drawn or modified ROI). The second menu option deletes ROI's with a name matching a specified template. A menu of possible ROI's that can be deleted are shown.

## 16.5 ROI analysis

It is possible to plot and export the following parameters over time:

- Mean signal intensity
- Standard deviation of signal intensity
- ROI area
- ROI area based on pixels
- Minimal signal intensity
- Maximal signal intensity

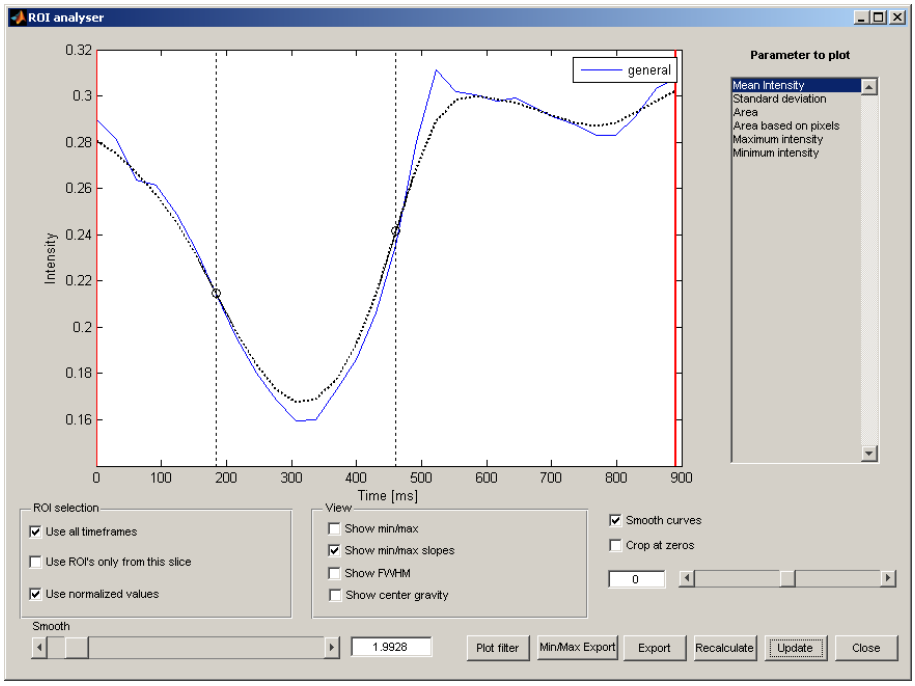



Figure 24: Graphical user interface for ROI analysis.

An example of the user interface is shown in Figure 24. In the ROI-selection panel the ROI's to plot can be selected. If the checkbox ☒ Use ROI's only from this slice is selected, then only ROI's in the current slice are shown. If the checkbox Use normalized values is selected the the values are shown in the `Segment's` own internal normalized representation. Otherwise the values are recalculated back to the pixel values in the DICOM files. In the View panel it is possible to select to plot min/max values, min/max slopes, or Full-Width-Half-Maximum (FWHM). If the checkbox ☒ Smooth curves is selected, then the curves are smoothed before slopes, and min/max values are calculated. The smoothing is applied is a Gaussian smoothing kernel. The smoothing parameter $\sigma$ is adjustable with the slider, and the edit box. By using the Plot filter button it is possible to plot the filter in the temporal domain. Currently the filter is applied directly to the ROI curve. Finally, the Export button exports all parameters to the clipboard. The Max/Min Export button exports the values and timing of min/max, min/max slopes, and FWHM. Note that that when changing plotting options the plot is not updated until you click Update.

## 16.6 ROI histogram

This function plots the histogram of ROI(s). When initiated the program asks for a selection criteria on what ROI's to include. If no ROI's are present then the histogram for the whole image (current slice and time frame) is displayed. The most common percentiles are also calculated and exported to clipboard. An example is shown in Figure 25.

## 16.7 Multiple threshold analysis

This function calculates the number of pixels inside the ROI's above the selected threshold. Before starting the program prompts for start threshold, end threshold and number of levels. All curves are plotted at the same level. The offset of each curve is displayed. All numeric data are copied to clipboard. There is also a visual mode where the pixels above a certain threshold are color-coded. An example of the visual analysis is shown in Figure 26. You are also prompted whether to use the internal normalized image pixel values or the original data from the file. The non-normalized range can be found by plotting the image intensity mapping (found under Image tools). By

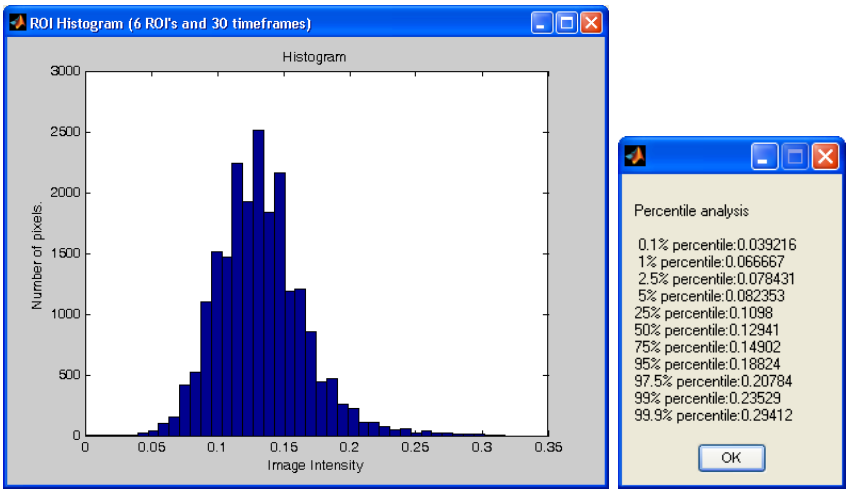



Figure 25: Example of ROI histogram.

selecting Multiple threshold analysis - numeric the same analysis is performed for each time frame and numeric values are exported to the clipboard.

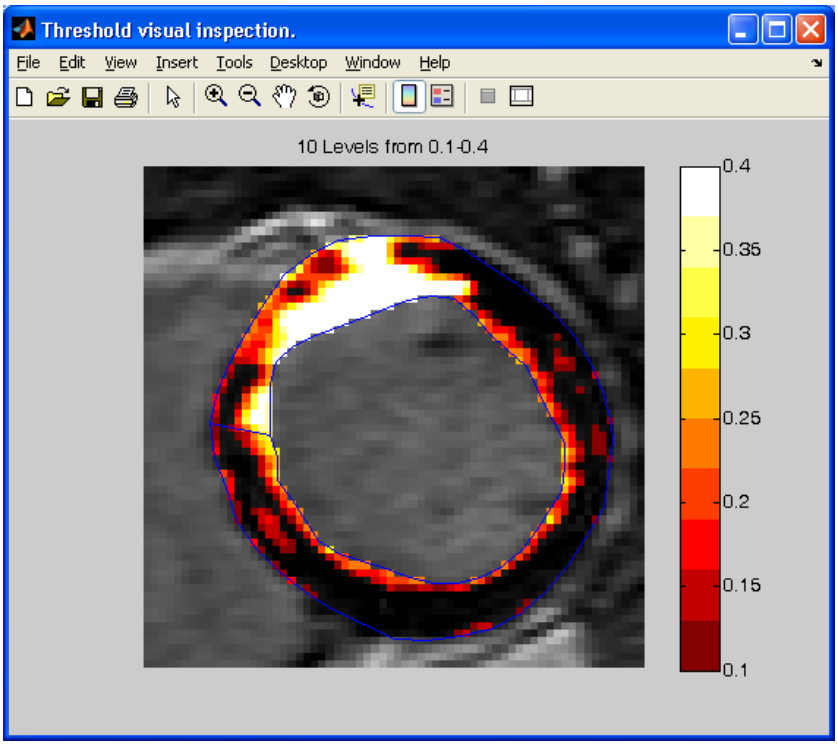



Figure 26: Example of multiple threshold analysis.

# 17 Measurements and Annotations

The whole software package Segment is designed for quantitative analysis and subsequently there are a rich variety of measurement tools available.

## 17.1 Length measurements

There are two possibilities to make length measurements. The easiest method is to use the measurement tool . To place a measurement left click with the mouse, hold mouse button down and drag mouse to the desired location. You are then asked to annotate and give the measurement a label. It is possible to refine the position of the measurement by click one of its end-points and drag that to the desired position. The measurement with its annotation is shown in Figure 27. Under the Annotations menu it is possible to clear or export all measurements to the clipboard. Measurements of ventricular wall thickness is best performed by using the tools for region wall motion analysis described in Chapter 22.

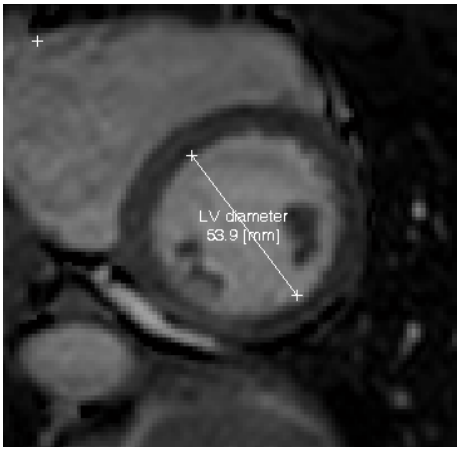



Figure 27: Example of a measurement of the left ventricle diameter.

Another method to get distances (or timing intervals) by adding annotation

points at different points in space and time. Annotation points are added with the icon and export the coordinates and time points of the annotation points to Excel or another spread sheet program and there calculate the distance. Annotation points is also useful for marking anatomical landmarks etc. For further details, see Section 17.7.

## 17.2 Timing

By using the M-mode viewing mode it is possible to make measurements of both timing and distances. This is illustrated in Figure 17, on page 51.

## 17.3 Volumes

Volume of the left ventricle is displayed and updated as soon as you have delineated some slices. Volumes of ROIs can be derived by using the numeric multiple threshold analysis described in Section 16.7. On possible mistake when doing manual delineation of the left ventricle in only diastole and systole is the failure to indicate what time frames that are end-diastole and systole respectively. This will cause `Segment` not to show any volumes. Selecting diastole and systole can be done by interactively dragging ED and ES in the volume graph or using the Autodetect End systole and End diastole under the Edit menu.

## 17.4 Area

Area of ROI's can be derived by using the region of interest analysis tool in Chapter 16. In certain cases area can also be derived by dividing volumes by the slice thickness. The area of the ROI's is shown for each ROI in the one slice view. In the near future a general area tool will also be added to Segment.

## 17.5 Flow and volumes

Measurements of flows and volumes are covered in Chapter 20.

## 17.6 Signal intensity

Signal intensity can be measured by using the region of interest analysis tools described in Chapter 16.

## 17.7 Annotation and anatomical landmarks

Annotations are added with the ABC icon or under the Annotation menu. The points can either be stationary or time resolved (i.e have different positions in different time frames). The stationary points are marked with a bold font. To make a pointtimeresolved right click on it and select Make point timeresolved from the pop-up menu. Note that this operation is undoable. It is possible to Clear All Annotation Points, Clear Annotation Points Using Template, Rename Annotations Using Template, and Export All Annotation Points. When deleting or renaming using a template you are prompted for a template. The template must be an exact match since no wildcards are allowed.

To propagate the location of a time resolved point, press `Ctrl-F`. Note that you need to have the annotation tool ABC active when doing this.

# 18 Utilities

The functions described in this chapter is off label use and for investigational use only.

The differentiation between a utility and a function/feature is that the utility does not necessary apply to an image stack. Currently there are five utilities available.

## 18.1 Anonymize DICOM files (Recursively)

This function ask for a folder of DICOM files and replaces the patient name with a new name for all the DICOM files. Caution since it overwrites the existing DICOM files, and it is recommended to backup these files prior to running this function. The function change PatientName and removes patientID, DateofBirth, OtherPatientIDs, EthinicGroup, Occupation, AdditionalPatientHistory, PatientComments, InstitutionAddress, and InstitutionName.

## 18.2 Anonymize `.mat` files (Recursively)

This function takes a folder of .mat files and anonymize the files and change the patient name to the filename of the .mat file. This function is particularly useful when anonymizing a complete research study.

## 18.3 Clear segmentation from multiple `.mat` files

This utility is useful when one want to clear the segmentation from multiple .mat files at once. One particular example when it is useful is when a second observer should reanalyse all files. In such cases copy all files, rename them and run this function.

## 18.4 Sort Folder of DICOM files

This utility is useful when you a have a large collection of DICOM files that are in a strange order. This is often the case from certain Siemens scanners. The program will sort them up in folders that are arranged as

patientname+patientid, studydate+stydyid, and series number. Each folder will contain sorted files according to instance number and trigger time.

The graphical user interface is shown in Figure 28.

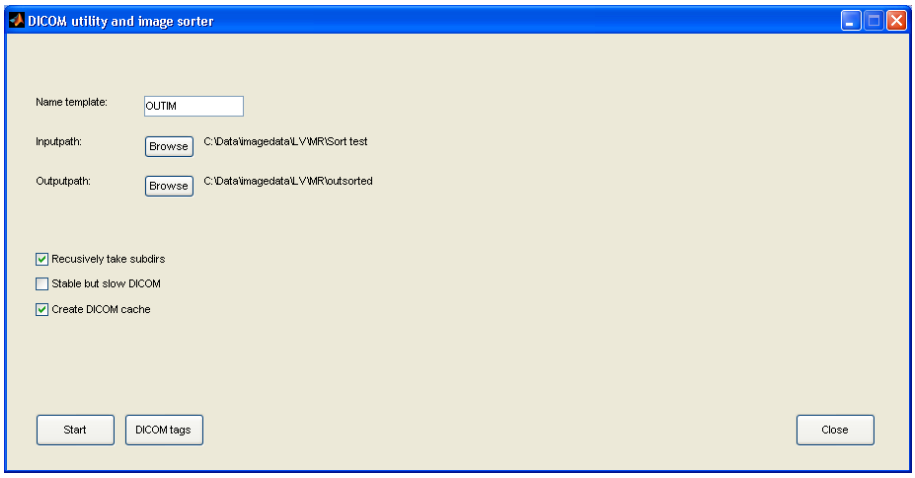



Figure 28: Graphical user interface for the DICOM sorter.

Start by selecting input and output folders/path/directories. If the checkbox ☒ Recursively take sub dirs is selected then the program will take all files below the selected input directory including its subdirectories. The input/output folders should preferably not overlap. Each file will be named according to the name template followed with a 5 digit number. The function DICOM tags asks for a filename and displays all DICOM tags in that particular file. The checkbox ☒ Stable but slow DICOM controls what DICOM interpreter is used in the sorting operation.

If you select the checkbox ☒ Create DICOM cache then the program will create cache files that are used when loading DICOM data into Segment. This will significantly speed up loading and is therefore recommended. For more details of caching of DICOM files, see Chapter 9.

## 18.5 Copy and Sort Images from CD to Data Folder

This function is ideal to use when you have images on a CD (structured or not) that you want to copy to your harddrive and subsequent analyze. This function assumes that you have set the location of your CD drive in the preferences (see Chapter 25). This function sorts and name the files in the same manner as the sorting utility. DICOM cache and thumbnails are also created.

## 18.6 Create DICOM cache for folders recursively

This function ask for a folder and creates DICOM cache files for all subdirectories. This functionality is highly useful when you have copied large sets of DICOM files to your local harddrive that you need to load into Segment. It takes a long time to run so a good idea is to start this function over lunch. Once this is done loading of your DICOM files will go much faster.

## 18.7 Create thumbnails preview recursively

Analog to creating of DICOM cache files but creates thumbnail preview for all subdirectories. Depending on the number of subfolders this function may also take quite long time to run.

## 18.8 Find patient details in .mat files

This utlity allows to scan your entire harddrive (or network drive) for patient details in .mat files. Output is a list of all patients occuring in the directory tree. This feature is useful when you want to ensure that you have not stored any sensitive information on your local computer/laptop for instance. The output is an Excel file where each row .mat file with patient information.

## 18.9 Find patient details in DICOM files

Analog to the above function, but instead looks in all your DICOM files. The following heuristics is used to classify a file as DICOM or not:

- Files that ends with `.dcm`.
- Files that only contains digits and no extension.

- Files with name that contains more than 7 dots and the two first letters corresponds DICOM identification of an imaging modality.
- `dicom.cache` files.

The output of this function is an Excel file where each line is one unique patient identity and the number of files in which the patient name was found. Note that to be completly certain about the are no DICOM files with the patient details you need to count the number of files that are deleted / anonymized for each patient or simply run the function twice.

## 18.10 Export from multiple `.mat` files

This function summarize multiple `.mat` files into one summary. This is very useful for research studies. For instance by placing `.mat` files, one for each patient in one folder. It is possible to summarize all patient data into one Excel sheet. Note that each `.mat` file can contain several image stacks. The program automatically determines what image stack is for instance short-axis slices, and what image stack is viability images. If this automatic image stack detection fails it may be necessary to load the image stacks and select correct image type. For further details see Section 15.13. Currently the following data is outputed for each files; File name, Patient name, Patient ID, Age, Length, Weight, Sex, BSA, Heart rate, R-R interval, LVM in ml, LVM in g, EDV, ESV, EF, LVM from viability images, Scar percentage, Scar in ml measured on viability images. Furthermore, for each ROI in the image stack the name of the ROI and the total volume is reported. When EDV, and ES is not exported see Section 17.3 for hints.

## 18.11 Export Information from multiple `.mat` files

This function exports imaging information from multiple `.mat` files. Example on exported information is:

- `ImageType`
- Image size
- Resolution
- Slice thickness and slice gap
- Time increment between

- Information whether the file contains infarct sizing, flow information, segmentation

# 19 Viability Analysis

The functions described in this chapter is off label use and for investigational use only.
The viability tools can be found under the MR menu in Segment. The method used for automated delineation of infarct is described in [4]. It uses a new paradigm in analyzing delayed contrast enhancement MRI. Instead of treating each pixel as dichotomously infarcted or not infarcted pixels are weighted with their signal intensity.

The new method delineates a larger area than the previous method [5]. It should be noted that even though it delineates a larger area, this should not be compared to manual delineation, since the darker pixels are given a lower weight. As a graphical illustration of this a pink line is also shown in the weighted mode. An example of this is illustraded in Figure 29. This line graphically represent the corresponding non weighted area. Please not that this line is only provided for visual feed-back and should not be used for any quantification purposes. The weighted scar delineation method is extensively validated in animals, computer phantoms and 40 patients on images acquired both on Siemens and Philips MRI scanners.

The first step to do viability analysis of delayed enhancement MRI (DE-MRI) images is to delineate both endo- and epicardium. This can be done either manually or by a semiautomated method. In many cases however, it may be faster to manually draw the endo- and epicardial contours. Then select Auto Delineate Viability (Weighted method) to delineate infarct. The automated delineated infarct is now shown with a yellow contour. After the delineation you can select the mode of operation. The default mode to use is the weighted automatic scar delineation (see below for details).

In the Viability menu you can select mode of operation, reset all scar delineation, reset user corrections, control visibility and automatic parameters. It is possible to add infarct regions by using the pen tool

and remove infarcts with the rubber tool regardless of the mode of scar delineation. The tool removes the manual corrections made with the

or . By default manually added scar regions shows up in green and manually deleted

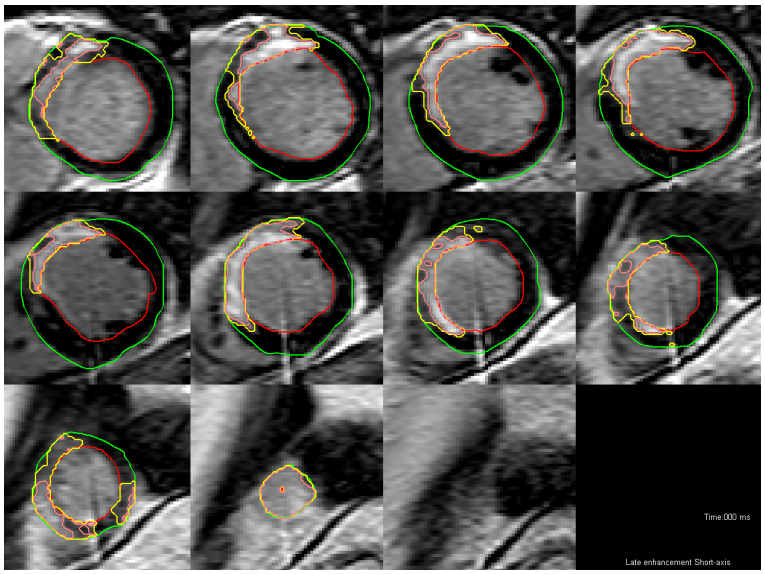



Figure 29: Example of scar delineation in the weighted mode. The yellow line denotes the complete affected area, and the pink line a graphical representation of the corresponding weighted area.

areas in blue. The tool is used to manually draw regions of microvascular obstruction. Microvascular obstruction is indicated in red. User interaction (and microvascular obstruction) can be showed/hided by clicking the key o. Note when using the weighted method, regions with microvascular obstruction needs to be manually drawn if not automatically detected, since otherwise they are weighted incorrectly. It is also possible to remove regions with microvascular obstruction with the toggable menu option Remove microvascular obstruction. Apex post processing is a technique described in [5] to handle case where the complete slice is infarcted. This functionality should normally be enabled.

The following modes of scar delineations is available:

- None. No viability, this will remove viability delineations.
- Manual mode. Manual drawing of hyper enhanced regions
- Automated Method (Weighted - default). Automatic scar delineation as described in [4].
- Automated Method (SCJ method). Automatic scar delineation as described in [5].
- SD from remote. Implementation of taking two 2-SD from remote myocardium as proposed by Kim *et. al* [6]. You need to place ROI's in the myocardium and label them ase 'remote'.
- K-means. Using the k-means algorithm, with two normal distributed classes (infarct and non infarct). Original algorithm described by [7].

Each of the different methods are further described below.

## 19.1 Automatic mode weighted or SCJ

The automatic mode is the default mode. In cases where it fails make necessary manual corrections by using the tools and respectively. Note that including extraneous black regions in the weighted method only marginally changes the result, since the infarct is weighted with pixel intensity. In the weighted method it may be necessary to manually mark regions of microvascular obstruction to get these regions weighted correctly.

## 19.2 Manual mode

In this manual mode the infarct area is not automatically updated and the only way to change the delineation is by doing manual interactions. If you want to start from scratch to manually draw your infarct regions, then first select Clear all scar data. This option also resets the viability mode to Automatic mode so you need to choose Manual mode before starting to draw the infarct regions.

## 19.3 SD from remote

It is possible to do scar delineation as proposed by Kim *et. al* where the infarct is determined as pixels with an image intensity that is higher than the mean plus two standard deviations from the mean in a non infarcted remote region. In the original method by Kim et al when one read the paper carefully they used two types of ROI's, both remote ROI's and also a scar region ROI in which the thresholding was applied. Therefore, the same approach is also applied in Segment.

To draw remote region use the ROI drawing tool or Add ROI's in sector under the ROI menu. The latter option adds ROI's in a sector in selected slices with a position specified as an angle, the width as and angle and finally the distance from the endo- and epicardium as percentage of the wall thickness. This option automatically flags the ROI's to be remote regions, but if you use the ROI drawing tool you need to manually flag that by right clicking on the ROI and select Select ROI label on the pop-up menu. When drawing a subsequent ROI the label of the ROI is copied from the last modified ROI so you only need to first draw one ROI, then label it and draw all remaining ROI's. If you do not draw a remote region in the threshold for that slice is then intra/extrapolated from adjacent slices. Using the default viability options this approach will only set a threshold to the level set algorithm based on the drawn ROI's.
To draw the scar region ROI's (Scar region ROI) use the same approach as described above. It is often advantagoues to first draw all the remote ROI's and then the scar ROI's since you do not need to alternate with labeling the ROI's.

In a final step to use the method of standard deviations from remote, you

need to set the parameter Beta to zero. To change the standard deviations from remote, see under Technical details below.

## 19.4 Technical details

It is possible to control the parameter Beta, Min volume, Standard deviation from remote. The parameter Beta controls the smoothness 'curvature' forces on the level set surface and in practice it controls the smoothness of the result. The parameter Min volume controls the minimum size allowed for an infarct in ml. The parameter Standard deviations from remote controls how many standard deviations from remote that should be taken when calculating a slice based threshold. The default for the automatic mode is 1.8 for the weighted algorithm, and 2.4 for the SCJ method. Generally this should only be changed when using the mode SD from remote. These parameters are further described in [5, 4].

# 20 Flow Analysis

This functionality may depend on your MRI scanner. Currently it has been tested using Siemens, Philips and GE scanners.

When flow image stacks are displayed, the screen should now similar to what is shown in Figure 30. On the left image panel the magnitude image is shown and on the right image panel the phase image is shown. When a flow image stack is selected a white frame around both the magnitude image and phase image is drawn in the thumbnail preview area. This helps to keep track of which phase images belongs to which magnitude images.

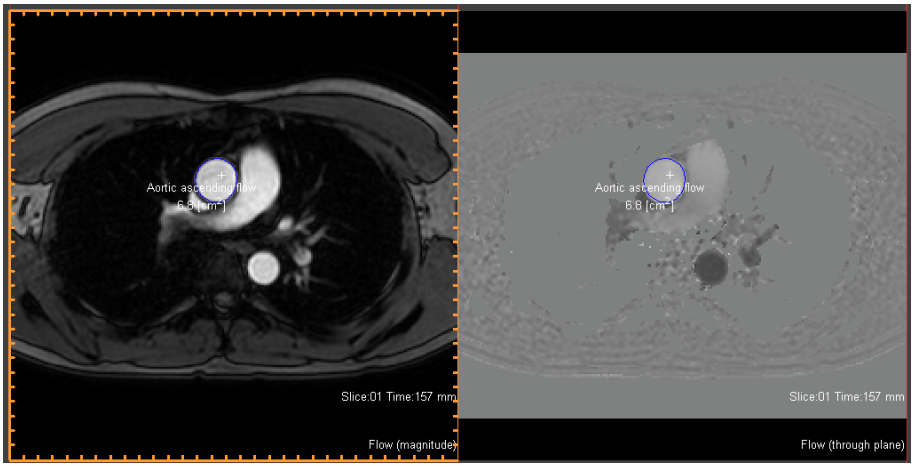



Figure 30: Example of main GUI in flow mode.

## 20.1 Automatic segmentation of flow ROI's

The suggested method is to select the ROI tool . Then draw a ruff outline of the vessel contour. Thereafter start the automated vessel tracking and refine. This is done by pressing `Ctrl-T`.

Another method to automatically segment a vessel is to drag the center cursor (white +) to the approximate center of the desired vessel and press `Ctrl-G`,

or Auto delineate a vessel under the Segmentation→ROI and Flow Tools menu. The vessel is automatically delineated and you are asked for an appropriate label. Deleting, renaming, recoloring the region of interest is described in Chapter 16. If you are not satisfied with the ROI there are two methods that can be applied.

### 20.1.1 Refine

Refine operation operates on the current time frame or all time frames depending on the checkbox ☒ Single frame mode. Short key for the refine function is `Ctrl-R`. You need to have the ROI pen active when using the hot key. Refine on all time frames is particularly useful if the vessel is fairly round and not to close to other surrounding tissue.

### 20.1.2 Refine and propagate

Start at the first time frame of the time series. If pleased with the result simply use the right arrow key on the keyboard to proceed to next time frame. When you find a time frame where you are not pleased with the segmentation use the ROI pen to adjust the contour or use the refine option Ctrl-R with the checkbox ☒ Single frame mode enabled. Continue by propagating the contour by pressing `Ctrl-F`.

### 20.1.3 Shrink flow ROI

If the RIO is outside the vessel then it might be advantageous to shrink the ROI followed by one ore more refine operations. Shrink flow ROI is found under the Segmentation menu and the submenu ROI and Flow tools.

## 20.2 Plotting the result of the flow analysis

The flow plotting utility is started by using the icon or by using the function Plot flow curves under the Flow menu. An example of the graphical user interface is shown in Figure 31.

In the upper right area of the GUI you can select which parameter to plot. The volumes presented in Volume panel of the GUI represents flow integrated between the two vertical red bars. These bar can interactively be moved with the mouse to control the range of the integration. Forward volume is the volume of the flow integrated only over the time frames where the

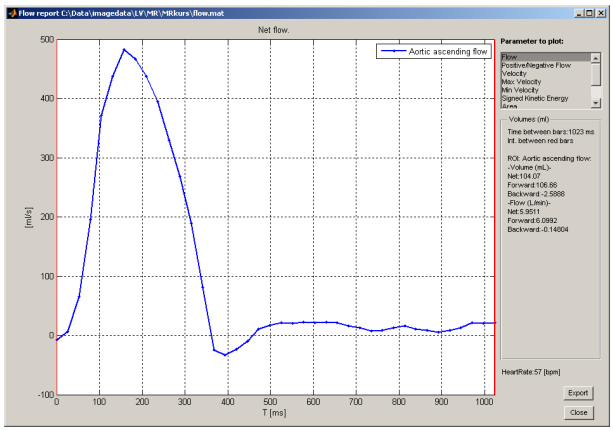



Figure 31: Example of flow plotting GUI. Plotting parameter can be selected in the upper right corner of the GUI. The flow integration is performed between the two red bars.

net flow is positive (forward). Backward volume is the volume of the flow integrated only over the time frames where the net flow is negative (backward). This should be contrasted to the flow parameter Forward/Backward that plots simultaneously the flow that goes forward and backward of the region of interest. Note that there can be significant backward flow in one time frame even though the net flow is forward in that very time frame. An example on the latter is shown in Figure 32. The sum of the two curves is the same as the net flow that is shown in Figure 31.

It is also possible to plot the Velocity over time, and this is shown in Figure 33. The 'error bars' denote the standard deviation of all pixels in the ROI of that particular time frame.

Another possibility is to plot the max or min velocity in the ROI over time. It is also possible to plot the radius and diameter over time. The radius are calculated as; what diameter need a circular vessel have to have the same area as the area of the ROI. The option Signed Kinetic Energy calculates the kinetic energy in the blood assuming standard density of the blood.

The final possibility is to plot a 3D profile of the velocity distribution of the vessel. This can be plotted for all time frames at once or only a single time

frame that later can be stepped forward/backward in time. An example of the 3D plot is shown in Figure 34.

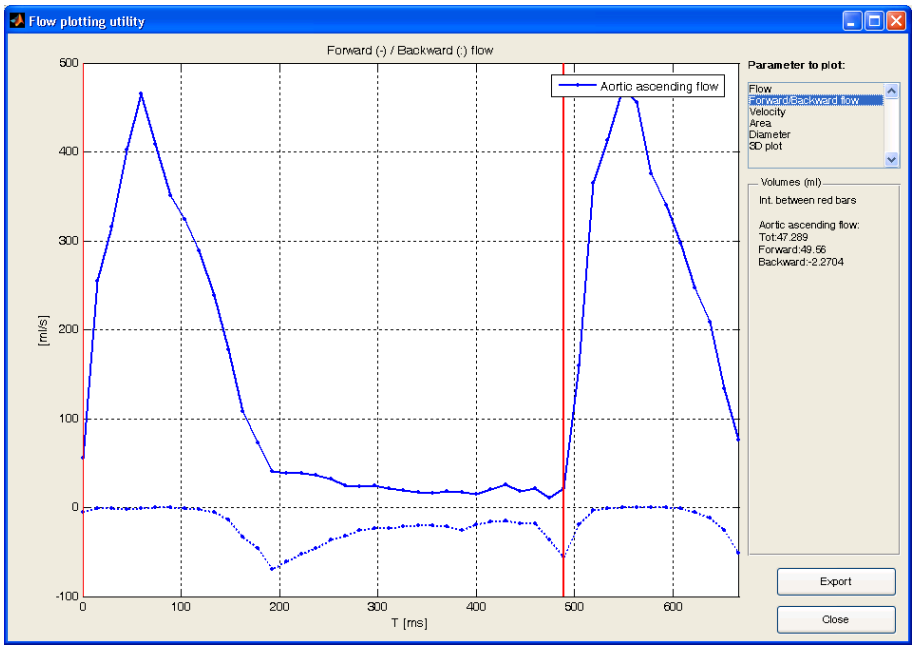



Figure 32: Example of plotting of backwards and forward flow simultaneously. The sum of the two curves will be the net flow showed in Figure 31.

## 20.3 Compensating for eddy current effects

To get accurate flow measurements it is important to compensate for concomitant field effects such as eddy currents, and Maxwell effects. Ideally Maxwell effects should be compensated for directly on the MRI scanner since it can be analytically calculated. Consult your MRI vendor for details about how this is implemented in your scanner. Note that when compensating for eddy current effects the image stack should not be cropped upon loading, since the algorithm need phase information of static tissue in the chest wall to function properly.

The graphical user interface for compensating for eddy current effects is shown in Figure 35.

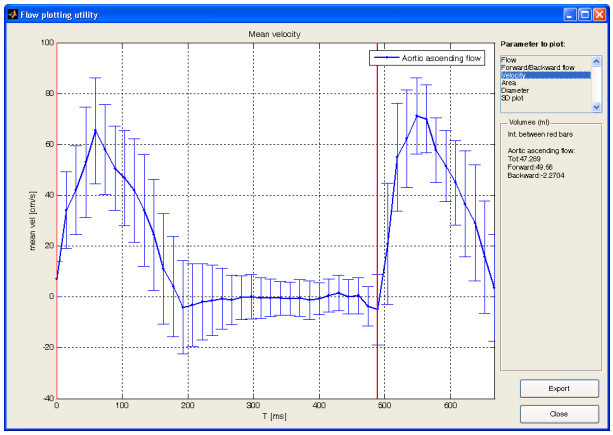



Figure 33: Example of plotting of velocity over time. The 'error' bars shown the standard deviation of the pixels within the ROI over time.

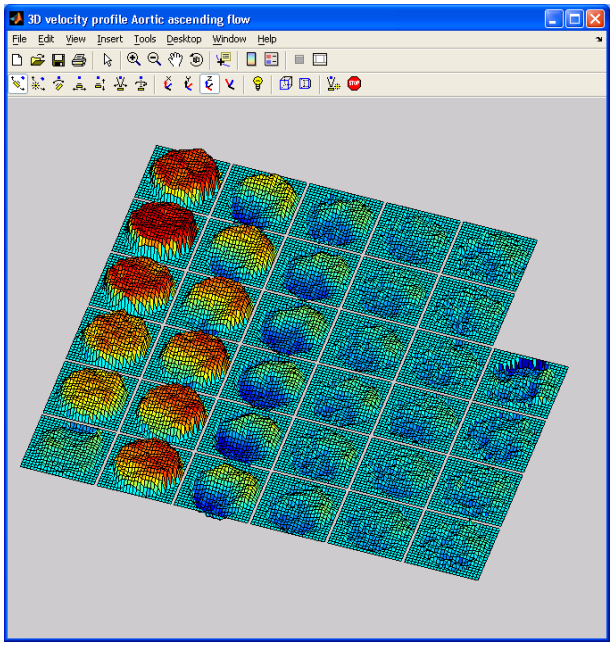



Figure 34: Example of plotting of a 3D profile of the velocity distribution.

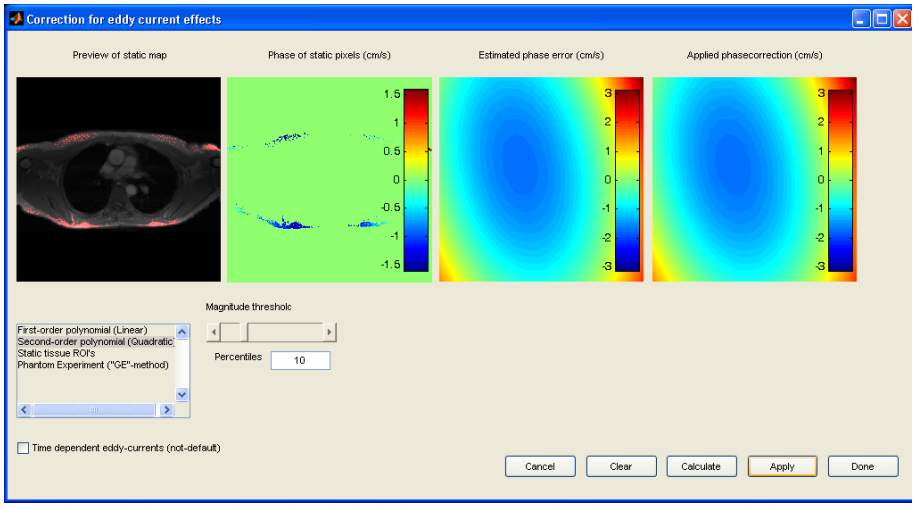



Figure 35: Example graphical user interface for compensating of concomitant field effects. In the left the identified static tissue is the displayed, and in the middle panel the corresponding phase for these pixels is shown, and in the right panel the resulting phase correction is shown.

You can select model order, and clear the phase correction. When you are pleased with the phase correction press Apply to proceed. The function automatically finds stationary parts in the image by selecting a percentage of the pixels whose standard deviation of the phase over time is smallest. The fraction of pixels taken can be controlled by the edit box Percentile. The image is divided into four quadrants and the algorithm to find stationary pixels is applied to each quadrant separately. This is done to ensure that there are about the same number of pixels from each quadrant. Pixels taken as stationary tissue are shown as red dots in the magnitude image. The Magnitude slider controls what magnitude the pixels need to have before being labeled as stationary. By selecting the mode of operation as Static tissue ROI then ROI's that are labeled Static tissue are taken as stationary areas. This is particularly useful when doing phantom experiments, since the automated identification of static areas fails in cases with stationary flow. The mode of operation `Phantom Experiment (GE-method)` automatically finds a flow image stacks that have the same scanning parameters this useful

when a static tissue have been scanned in the same position as the patient as recommended by GE for eddy current compensation. For usage, see paper by Alex Chernobelsky *et al.* [8].

## 20.4 Phase unwrapping

In cases were the velocity in the blood is higher than the VENC the velocities can wrap around. Under certain conditions these phase wraps can be uncovered and phase unwrapping can be performed to retrieve the correct velocities. The graphical user interface for the phase unwrapping tool is shown in Figure 36.

The checkbox ☒ Show ROI pixels shows the pixels that are used in the ROI in a red color. This is useful when one want to know exactly what pixels are included in the ROI. The checkbox ☒ Use magnitude mask is used when one want to limit the automated phase unwrapping only in pixels that have a magnitude over a certain threshold.

### 20.4.1 Automated unwrapping

The automated phase unwrapping algorithm works on a pixel by pixel basis and operates along the temporal dimension. It looks for pixels where the phase appears to have wrapped once up and once down. Therefore the algorithm will fail for a biphasic velocity profile if phase wrapping occurs at both phases. Furthermore, it only considers single wrap arounds (i.e the phase is assumed to have wrapped once).

### 20.4.2 Manual unwrapping

There are four tools available, . The tool  is used to pan the images. The second tool  wraps the pixel up at left mouse button clicks. The third tool  wraps the pixel down at left mouse button clicks. The fourth tool  is used to plot the phase of the current pixel over time. This is mainly useful for debugging purposes. It is possible to zoom the image by usage of the zoom icons . Undo last operation is done by pressing `Ctrl-Z` or the icon .

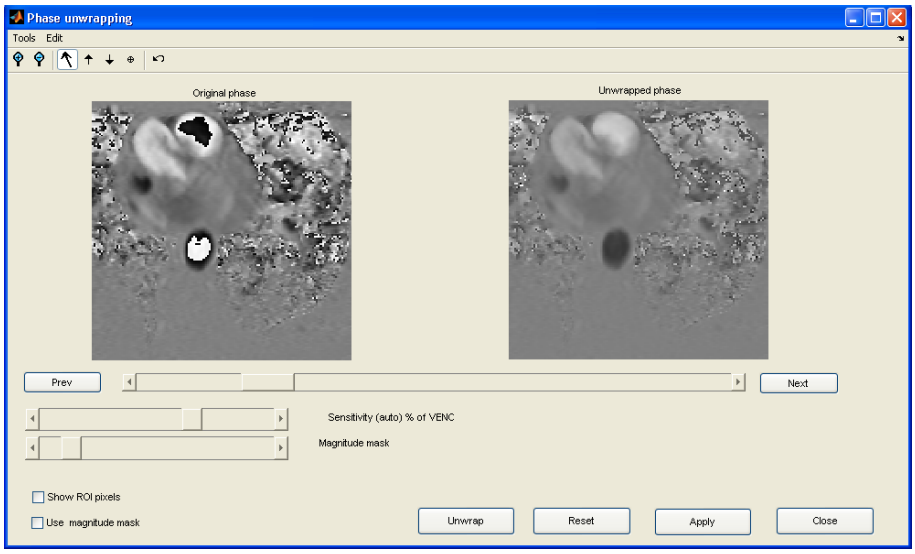



Figure 36: Example of the graphical user interface for phase unwrapping. The left image panel shows the original phase, and the right image panel shows the unwrapped phase. The long slider adjusts the current time frame.

## 20.5 Creating angio and velocity magnitude images

It is possible to create a so called angio image that is the magnitude image times the velocity magnitude. This is available under the Flow menu and Create Angio. If you have more than one velocity encoding direction it is possible to create a velocity magnitude image that is the square root of the sum of squares of all velocity directions (velocity magnitude).

# 21 Stress Analysis

In earlier versions of Segment there were a special stress viewer available. This have been removed since it's functionality is now directly available in the normal viewing capabilities of Segment (synchronized viewing of several image stacks). It is possible to place four (or more) image stacks on the screen simultaneously and play them synchronized in the same speed by the icon . Other functionality in Segment that could be used to analyse stress images is the report per slice functionality, described in Section 22.2 which allows quantitative studies of wall motion abnormalities.

Further hints on doing stress analysis is to label your image stacks. Then it is easy for the viewer to see which image stack is stress and which is rest. This is done by right click on the image thumbnail and select Set Image Type in the pop-up menu.

# 22 Regional Wall Analysis

There are a number of different analysis options available to make regional wall analysis. Please note that for regional wall motion analysis the common clinical practice is to exclude the papillaries from the segmentation, for more information on how to include/exclude the papillaries, see Section 11.3.

There are three different visualization options available for wall motion analysis:

- Radial contraction versus time
- Report per slice (icon )
- Bullseye plots (icon )

## 22.1 Radial contraction versus time

In this option the regional contraction velocity per segment is plotted over time. On the y-axis on each plot is the slices (basal to apical), and on the x-axis is time. An example is shown in Figure 37.

## 22.2 Report per slice

It is possible to do regional wall motion analysis on a slice by slice basis. This tool is started by the icon . Possible parameters to plot are wall thickness, fractional wall thickening, radial contraction velocity, and radius. An example showing wall thickness over time is shown in Figure 38. You can adjust the start of the sectors by using the rotation slider or take the starting sector as the sector that is closes to the annotation point `Start Sector`. How to place annotations, see Section 17.7.

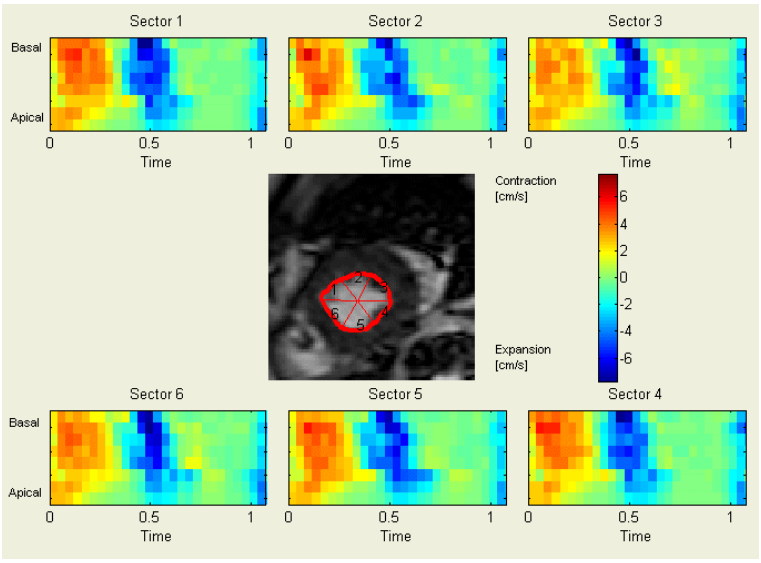



Figure 37: Radial velocity versus time in six sectors. Note the apical to basal gradient in the onset of the radial contraction.

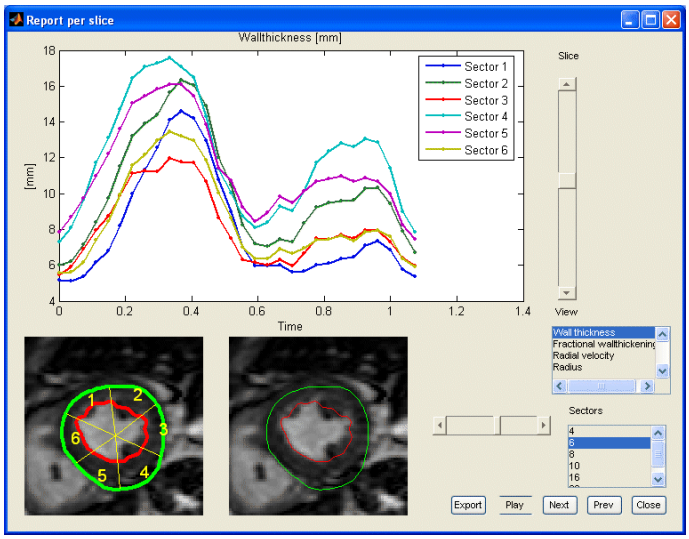



Figure 38: Wall thickness over time in a healthy subject.

## 22.3 Bulls eye plots

The parameters that currently can be plotted as bulls eye plots are:

- Maximal expansion velocity
- Maximal contraction velocity
- Expansion velocity at PFR
- Contraction velocity at PER
- Maximal wall thickness
- ED wall thickness
- ES wall thickness
- Wall thickening (difference wall thickness ES-ED)
- Fractional wall thickness
- Myocardium volume
- Scar transmurality
- Data from clipboard (each row is one slice, and each column a sector)

The graphical user interface for creating bulls eye plot is shown in Figure 39. The orientation of the bulls eye plot can be adjusted by a slider, and the number of sectors with a list box. **Note:** it is important to adjust the rotation correctly, so that the sectors corresponds with the correct anatomy. For correct AHA plots, one need to adjust the rotation so that the longest spoke in the lower right part of the GUI points to the middle of Septum wall.

It is also possible to export the results of the bulls eye plot to clipboard (to later past it into for instance Microsoft Excel). Note that only selected slices are plotted in the bulls eye plot. For further improve flexibility of editing and exporting it is possible to plot the bulls eye plot in a separate window. There are three possible modes of bulls eye plots, one with regular with uniform sectors displaying the 'mean' or nominal value for each sector, and one mode where the bulls eye plot is smoothed, and the final mode where the data is presented according to the AHA association model [9]. In order to make the AHA presentation meaningful you should have selected the whole LV. The smoothed bulls eye plot is done using cubic interpolation over Cartesian coordinates. The possibility to plot data from the clipboard enables to plot data as bulls-eye plots that was not created with Segment.

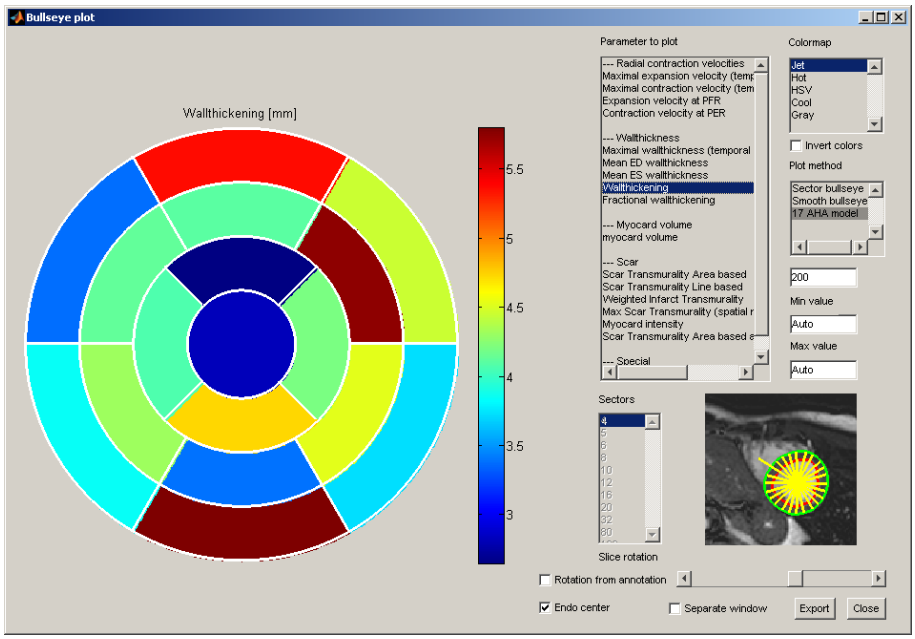



Figure 39: GUI used to create bullseye plots.

# 23 Export Images and Results

There are many options to do batch exporting from multiple `.mat` files. Please see Chapter 18 for further details.

## 23.1 Export results to clipboard

These functions export results such as LV mass, ejection fraction, volumes etc, to the clipboard. Data is outputed in a format so that it directly can be pasted into Microsoft Excel (by usage of `Ctrl-V` in Excel) or other spread sheet softwares. When you need to export data from multiple files, it is strongly recommended to use the utility to summarize `.mat` files described in Section 18.10.

### 23.1.1 All stacks with header

This function exports the results of all image stacks and includes a header line above. Segment tries to use the image type to determine which image stacks are short axis cine images which are used for mass and ejection fraction, flow image stacks, delayed enhancement image stacks and so forth.

### 23.1.2 All stacks

Same as above but no header line is included in the output.

### 23.1.3 This stack with header

This function only outputs results from the current image stack and includes a header line.

### 23.1.4 This stack

Same as above but without including a header line.

## 23.2 Export volume curve to clipboard

The volume curve (both) endocardial volume, and epicardial volume is copied into two columns.

## 23.3 Export contour to clipboard

This function ask what contours to export and export the internal representation to the clipboard. You can currently chose to export LV endo-, epicardium, RV endo- and epicardium, respectively.

## 23.4 Export volume of contours per slice

This function export the volume of each contour per slice. Data is exported for all contours and all time frames. If you instead want to have the area per slice you can divide the result with the slice thickness in cm to get the area in $cm^3$.

## 23.5 Export image

Using this option, only the current frame without segmentation is exported as a file. You need to select file format, and the following formats are supported: `.jpg`, `.bmp`, `.png` (portable network graphics), and `.tiff`. The recommended image format to use is `.png`.

Another alternative that often is very effective is to use screen-shots. The easiest way to do this is to use the Windows built in function by pressing `Alt-PrtSc`, that creates a screen-shot of the current window, and places that on the clip-board so that it is easy to copy that screen-shot to Microsoft Word or Power Point for instance. When preparing images for publication it is often helpful to change the color of the contours to black/white and increase line width to increase visibility. This can be done under the preferences menu, see Chapter 25 for further details.

## 23.6 Export movies

Exporting movies can be done by either using the built-in movie recorder in Segment or by exporting the current image stack as a movie (Export Movie).

## 23.7 Movie Recorder

This is an experimental functionality that take screen captures and store them in a movie format. The movies can be done in two ways and either to

`.avi`-files or a sequence of `.png` files (that later can be converted to different file formats). In future versions it will also be possible to export to animated `.gif` format. You can create movies of the main view, zoom view, 3D plot view, report per slice view. First select Movie Recorder under the Export menu. This brings up a user interface shown in Figure 40.

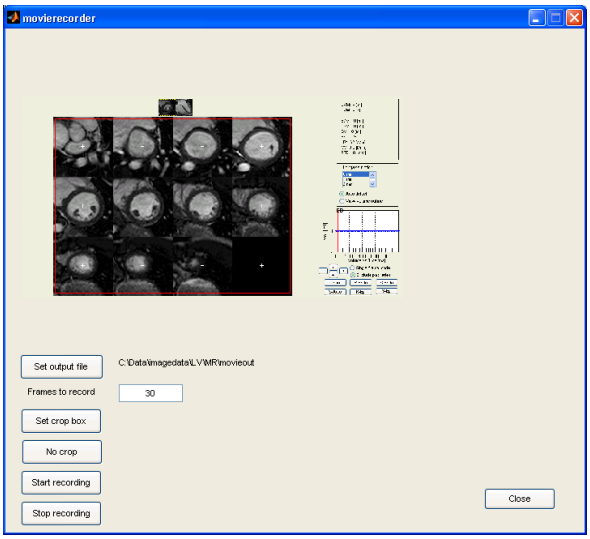
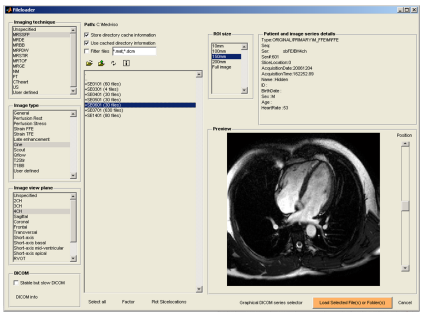



Figure 40: Movie Recorder GUI.

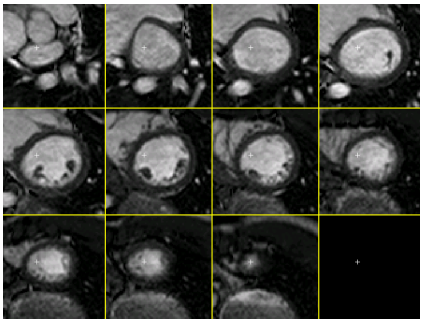
The movie recorder is when started unpopulated. To do a first screen capture force an image update by view next frame. You can now set a crop box (shown in Figure 40 as a red box), set number of frames to record, and start to record the movie. Usually you should set the number of frames to record to the same number of time frames as there are frames in the image stack. When all frames are recorded then a file selection pop up menu appears and where you can select storing options. When exporting to `.avi` files you need also to select a movie compressor, since all compressors might not be available on your computer. Personal experiences are that the cine-pak encoder are pretty stable.

# 24 LV Segmentation Example

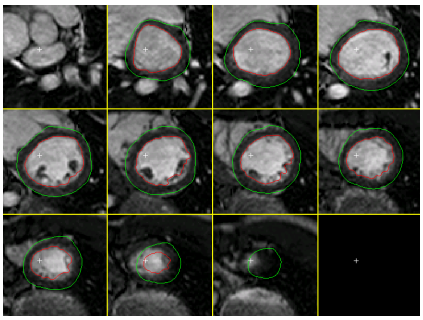
This example can serve as a fast introduction to the LV automated delineation tools in Segment. The example is chosen such as the segmentation result is not perfect, and thus illustrates how to make manual interactions to correct the segmentation.



Start by loading the dataset `ex1_mr_ssfp.mat` supplied with the example patient database.



To view the image stack as a movie, press the icon . This gives an overview of the image stack. The most apical slice is missing in this image stack unfortunately (was not included in the scanning). The most basal slice contains only left atrial parts in all parts of the heart cycle. Select all slices but the most basal slice.

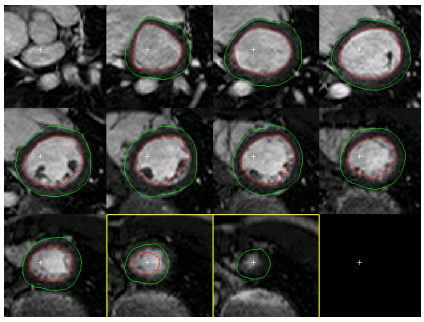


Start the segmentation by pressing the icon in the toolpalette, you need to be in LV mode to find the icon.

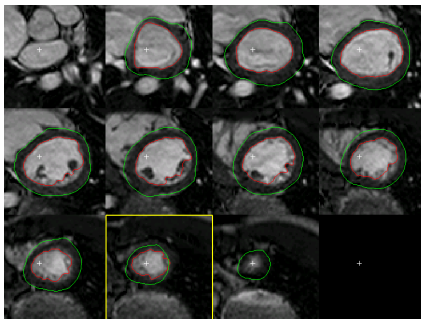
Show the segmentation by again playing a movie. You will probably want to

do some corrections described below:

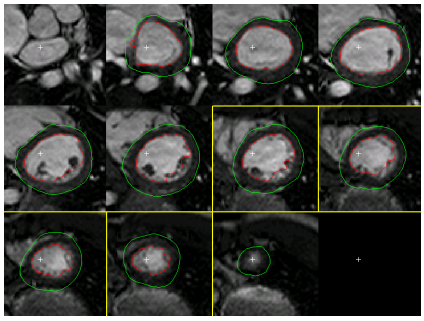
Misalignment of the two most apical slices. This is due to that the ventricle was not perfectly resampled into short axis slices. Correct this by selecting the drag tool ✣ and drag the segmentation result to the desired location.



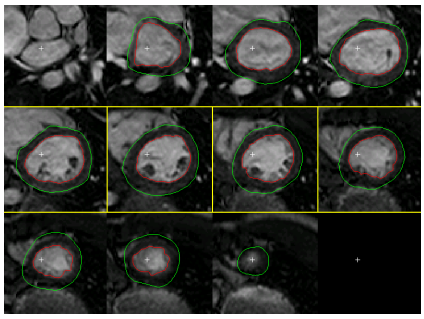
The endocardium for the second most apical slice needs to be refined (due to the same misalignment). Press `Ctrl-R` (refine endocardium) a number of times (each time the computer refines the endocardial segmentation slightly). You may also press `Ctrl-M` to redo the endocardial segmentation in this slice.

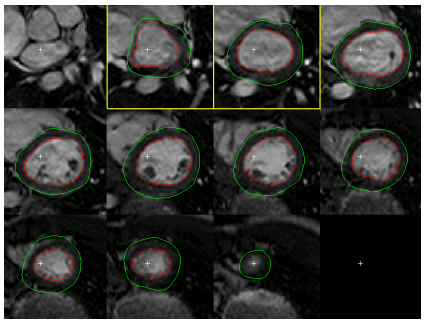


Now the epicardium of that slice needs to be fixed. The best method is to redo the segmentation in several adjacent slices to use as much image information as possible.



Some of the midventricular slices have problems with the papillary muscles get involved in the segmentation. Select these three slices, and press `Ctrl-V` (remove papillary muscles). Then press `Ctrl-R` (refine endocardium to get the endocardium to really follow the endocardial surface). This process of `Ctrl-V`, and `Ctrl-R` might need to be repeated once or twice. Twice is required for this image stack.





The two most basal slices have small problems where the endocardium goes into the wall. Correct them by selecting them and press `Ctrl-R` (twice is required).

There are many more possible corrections, for more details see the section about editing.

Now select a suitable long-axis motion. Unselect the Auto Detect radio button, and select view volume outline. Go to systole by pressing `S` on the keyboard. Select long-axis motion in the list box until you find an outline that you like. Only a fraction of the second most basal slice should be counted so maybe a long-axis motion of about 12mm or so should be adequate. To switch back to diastole press `D`.

# 25 Customizing Segment

This chapter describes how to customize Segment. It is recommended to set the preferences of which folders to use to avoid browsing each time you want to load or save a file. The GUI for setting preferences is shown in Figure 41. It is invoked by using the menu Preferences on the main menu.

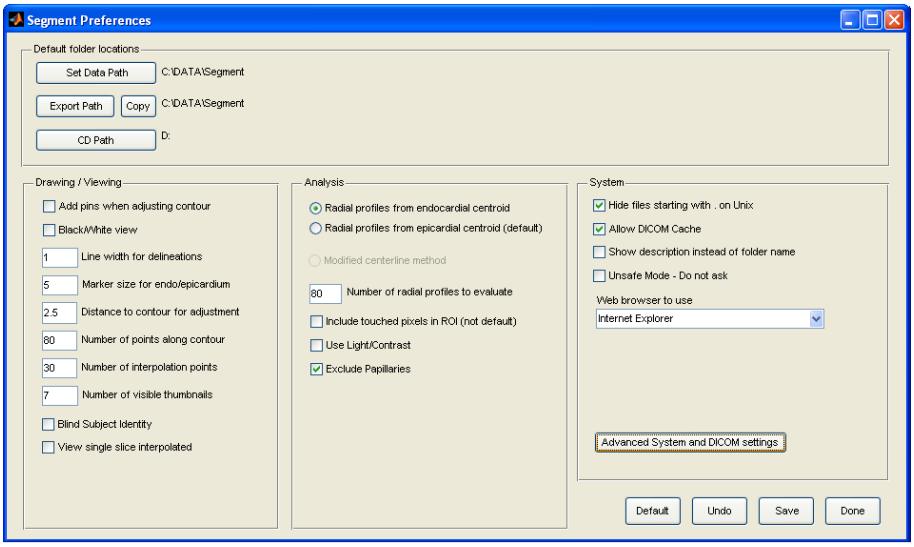



Figure 41: Preferences GUI.

There are four panels in total. The top most panels sets default folder locations for loading, and saving, respectively. It is also possible to indicate which drive / path that corresponds to your CD-drive. Then, the left most panel sets preferences for editing and drawing contours, the middle panel sets preferences for regional analysis, and the right most panel sets system preferences. The button Advanced System and DICOM Settings opens a new interface with settings for base image path for patient database, and DICOM communication parameters.

The option ☒ Add pins when adjusting contour controls weather points should be placed when manually correcting a contour. This option should be checked

when modifying time resolved images, but unchecked otherwise. ☒ Black/White view plots the endocardium and epicardium with white lines. This is useful for making screen captures for illustrations that are not printed in color. The edit box `Line width for endo/epicardium` sets line width for the contours. This again is useful for making screen captures. Default line width is 1. The edit box `Distance to contour for adjustment` adjust how close to a contour one need to click before this contour is activate. When using the interpolate tool it is recommended to set this to quite small, typically 1-2. The edit box `Number of Points Along Contour` sets the number of points that are stored along a contour for endocardium and epicardium. When using automated segmentation this value should be set to 80. When manually drawing complicated objects this can be set to a higher number.If the option ☒ Blind Subject Identity is checked then the program will not show patient info on screen this is useful for making screen shots etc for presentations. It is highly useful when doing research and the observer should be blinded to the patient identity. The edit box `Number of visible thumbnails` sets the maximum number of thumbnails visible. When the number of image stacks exceeds this number a slider will be visible to scroll through all the thumbnails.

The radio buttons `Radial profiles from endo/epicardial centroid` controls how regional wall measures are placed. The radio button ◎ Modified centerline method is reserved for future use when the modified centerline method will be implemented. The edit box `Number of radial profiles to evaluate` sets the number of radial spikes that are evaluated before sector means are calculated. For more details on how the regional parameters are calculated see Chapter 27. The checkbox ☒ Include touched pixels in ROI sets how the edge pixels of a ROI are treated. When selected all pixels that are touched by the ROI are included. The default behavior is to include only the pixels where the center of the pixel lies within the ROI.
The checkbox ☒ Allow DICOM cache allows creation of cache files for tags in DICOM files to be generated. The web browser to be used can be chosen in the drop list by either choosing a program if it is installed in the default location or choose other to browse for the program file to use for example select chrome.exe.
The graphical interface for advanced settings is shown in Figure 42. The checkbox ☒ Force 16 bit DICOM enforces Segment to assume usage of 16 bit DICOM files, regardless what is stated in the file. This option is helpful

when images looks like chessboard when read into Segment. For further details see about loading DICOM files in Chapter 9. The settings DICOM Prot, AE Title and retrieve mode are used to set up PACS module and Segment Server, more on these settings is found in the Chapter 37. The box titled `Define PACS servers` is used to define the external PACS servers that Segmentcan communicate with. When adding or editing a connection the following options are presented.

- `DescriptiveName`
- `Called_AE`
- `Peer_IP`
- `Peer_Port`
- `Port`

The `DescriptiveName` is just the name that Segmentuses to identify the connection. The `Called_AE` is the AE of the external PACS server. The `Peer_IP` is the IP address of the external PACS server and the `Peer_Port` is the TCP port of the external PACS server. Finally `Port` is the port used for the image transfer.

## 25.1 Technical details

On Windows platform, the preferences are stored under the local user folder and the subdirectory `Application Data/Segment`. This means that each user have can set their own preferences. If you want to have it setup so that all new users on the computer will have a default setting of preferences, then copy the `preferences.mat` from one user to the folder where Segment is installed. Finally make this file write protected. In the preferences folder Segment also stores a log file for debugging purposes, and small temporary files that are used in the PACS communication batchdownload process.

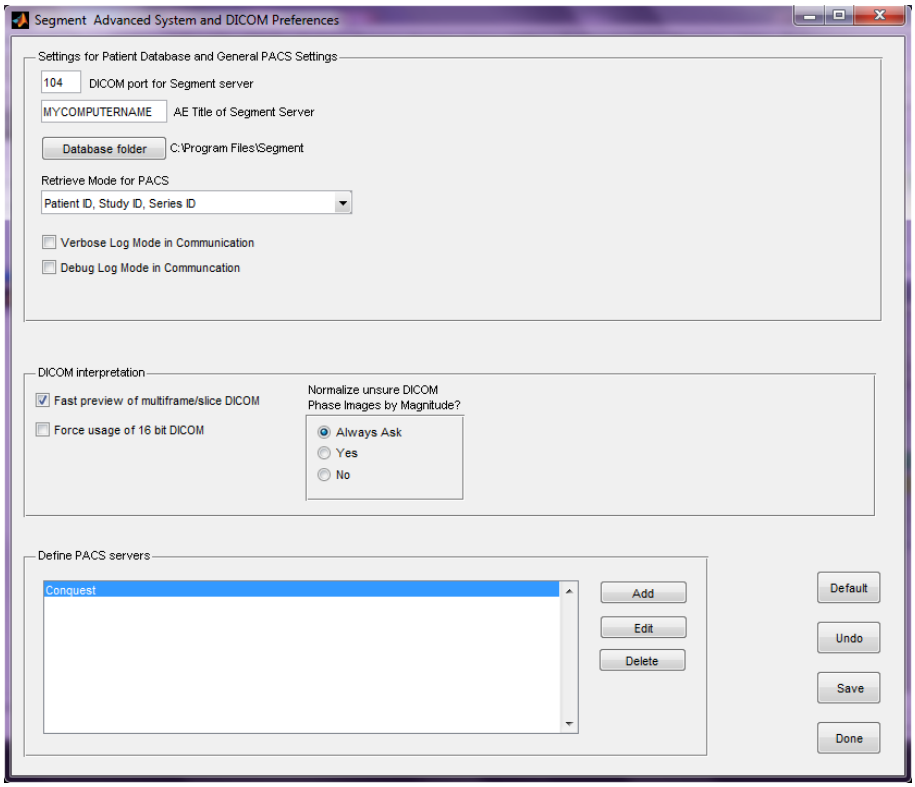



Figure 42: Preferences GUI.

# 26 Image Reformat (MPR)

The functions described in this chapter is off label use and for investigational use only.

It is possible to reformat an image stack along any axis. The main purpose of this tool is to be able to resample the data volume to short axis slices (if they are for instance scanned in an axial direction). The reformater can also be used to construct a long-axis image from a stack of short-axis slices. The user interface is shown in Figure 43.

One limitation with the multiplanar reconstruction is that it does not utilize the patient image coordinate system. This means that image stacks created with the reformater does not display image plane crossings. This will be addressed in future versions of Segment. Furthermore, the MPR routine does not currently support non-isotropical voxels (i.e voxels of dimension 3x4x8 mm). Voxels where x and y size are equal do work, i.e 3x3x8 mm works fine.
The functionality are:

| | |
|---|---|
| New cut | Resamples into parallel slices to the selected line. The cuts are also perpendicular to the viewing direction. |
| Previous cut | Backs up one level in the cut history. The current cut is not saved. |
| Done/Export | Exports the resample image stack back to Segment. |
| Play | Then this toggle button is selected then the image is played as a movie. |
| Close | Closes the dialog resampler without storing any information. |

Parameter slice determines the slice distance in mm, and output determines

the output resolution in the new 'short-axis' plane. This functionality is under development and not sufficiently validated. Please let us know if you would like to use this functionality in your research.

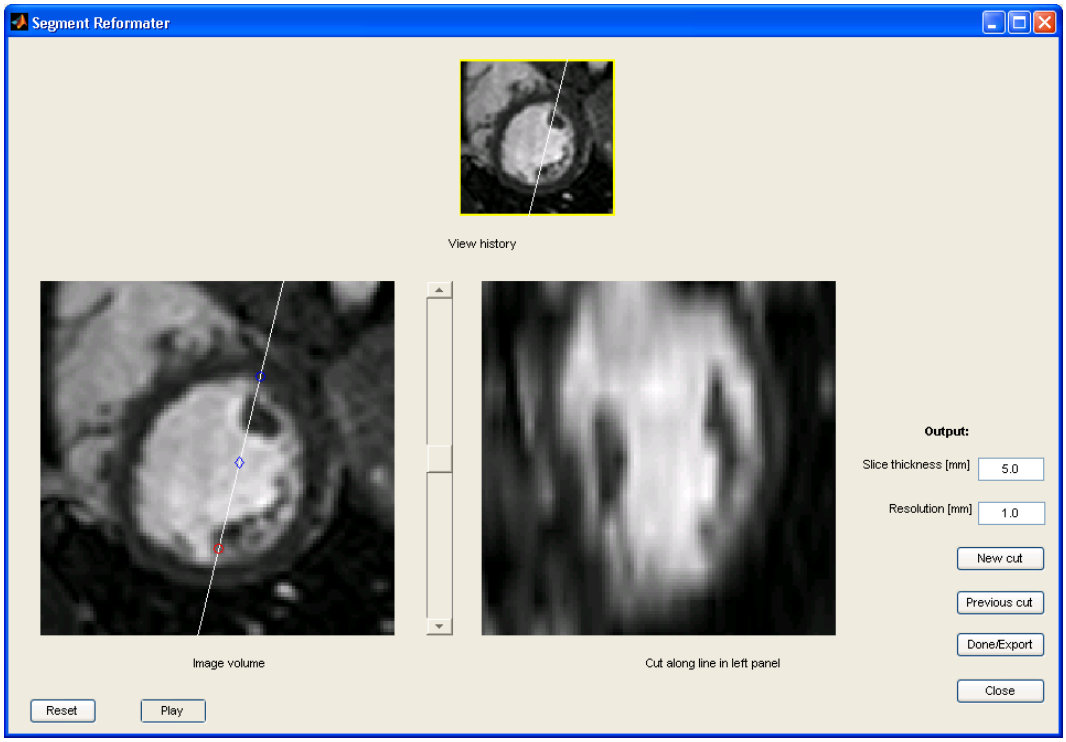



Figure 43: Image reformater GUI.

# 27 Implementation Details

In this chapter a few implementation details are given. There are much more details that are interesting, but this is as far as we have got with the documentation. If you have specific questions, please do not hesitate to ask us.

## 27.1 Version handeling

A proper version handling is employed when developing Segment. A detailed version history of Segment is available on the homepage `http://segment.heiberg.se/version.htm`. Upto version 1.7 this version control was manually, now SVN with Tortoise as a front-end is used. For more detailed version history, please see the revision log of Segment SVN.

## 27.2 Numeric representations

All numbers are stored and used internally as double precision floating points with the following exceptions:

- Images are stored as single floats (normalized) or as integers (uint8), and then as they are stored in the DICOM files. Most functions in Segment will automatically convert the data to floats.
- Edge detection results are stored as integers (16 bits, 'normalized')
- Character strings are stored in 8bit ASCII format
- Infarct maps are stored as int8 (manual interaction), and uint8 (result).
- General segmentation tool store objects as levelset function with an uint8 representation where the zero levelset resides at 128.

Internally the image stack is normalized upon loading by a global maximum intensity such that all values are [0..1]. Offset and scaling is also calculated so that the image stack can be reconverted back to original signal intensities.

## 27.3 Loading data and interpretation of DICOM tags

This section describes how Segment interprets DICOM information to calculate important parameters suchs as geometric properties of the images.

- Number of slices. This is calculated from the presence of different slices based on the DICOM tags `ImagePosition` and `ImageOrientation`.
- Number of timeframes. This is based on dividing the total number of images with the number of slices.
- Time increment in ms between each timeframe. This is based on the difference between the number of timeframes divided by largest and the smallest value of the DICOM tag `TriggerTime`. If the DICOM tag `TriggerTime` is not present then the DICOM tag `TR` is used as time increment. Note that this might depent on your k-space acquisition scheme so for scanners that do not report `TriggerTime` you really need to double check the estimated value of time increment.
- Heart rate. The heart rate is taken from the DICOM tag `HeartRate` if present. Note that many vendors (including Siemens) does not specify this. As a fall back Segment tries to calculate the heart rate assuming full R-R intervall coverage by using of trigger time (i.e it does not working for prospective imaging series). For long image acquisitions where one image is taken approximately for each heart beat then the heart rate is taken as the time between start of image acquisition and end of image acquisition adjusted for the number of frames. Note that in many cases this heart rate calculation will fail. Heart rate can be adjusted under patient details. Note also that heart rate may vary between image stacks therefore do not press Apply for all when manually changing heart rate. Heart rate is not used in any calculaion, instead time increment between image frames is used in all calculations.
- Slice thickness in mm. The slice thickness is taken from the DICOM tag `SliceThickness`. If this tag is not present then the information is taken from same DICOM tags as number of slices, and assuming slice gap to be 0.
- Gap between slices in mm. This is taken from the DICOM tag `Spacing BetweenSlices`.
- Pixelspacing in X-direction in mm (vertical direction in Segment). This is taken from the DICOM tag `PixelSpacing`.

- Pixelspacing in X-direction in mm (horisontal direction in Segment). This is taken from the DICOM tag `PixelSpacing`.
- Velocity encoding (VENC) in cm/s. For non velocity encoded images this should be 0. How this is interpretated involvs proprietry information of different scanner vender information.
- Rotated image stack. This should by default be false. If your image stack is rotated, then change this to true. Currently this parameter is not taken from information in the DICOM tags and the user needs to manually change this when loading rotated image stacks.
- Cyclic image. If the image stack is cyclic, i.e covers the whole heart cycle this should be true (default). For prospectively gated image series this should be false. This affects mainly the automated segmentatin algorithm. Currently this information is not read from the DICOM information.

## 27.4 Segmentation algorithm

The method is more completely documented in Paper IV in the PhD thesis by Einar Heiberg [10].

The segmentation algorithm used by the program is a truly three-dimensional and time resolved deformable model specially adopted for segmentation of the left ventricle. Blood pool signal intensity is estimated from a user selected center point (see manually edit segmentation result). From this manually selected point the contour is initialized as a small time-resolved tube, and the contour of the tube is expanded until it reaches edges or when the local image intensity significantly changes from the estimated blood pool signal intensity.

## 27.5 Volume calculations

The volume calculations are done by a summing the area in each slice. The main reason for not using a more advanced volume integration method is that no one else is using that and therefore it might be difficult to compare the results. Segmentation (i.e. delineation of endocardium and epicardium) is stored on a sub-pixel accuracy and subsequent calculations are on a sub-pixel basis. For viability the classification into viable or scar is done on a

pixel-wise basis and there the volume calculations are done by summing the number of pixels.

For the rotated image stacks the volume is given by a integration method. The volume contribution of each outline is given by :

$$\delta V = \frac{\pi}{2 * Z} \int y(s)^2 \texttt{sign}(y(s)) \frac{dy}{ds} ds \tag{1}$$

where the curve is given on a parametric representation $(x(s), y(s))$, $Z$ is the number of slices in the rotated image stack. No long-axis compensation is performed for the rotated image stacks.

## 27.6 Mass calculations

When converting volume to mass the density is assumed to be 1.05 g/ml. Note that this number differs in the literature between 1.04 to 1.05. Furthermore, note that these numbers are valid for healthy myocardium ex-vivo, what happens in for instance infarcted regions is not shown in the literature. Therefore usually it is better to report volume instead of mass.

## 27.7 Calculation of BSA

The formula used is based on Graham and George.

$$BSE = w^{0.51456} * h^{0.42246} * 0.02350 \tag{2}$$

where $w$ is the body weight in kg, and $h$ is heigh in cm.

## 27.8 Peak ejection/filling Rate

When calculating peak ejection and peak filling rate the volume curve is differentiated using forward difference approximation. For cyclic datasets cyclic convolution is used for the calculation.

## 27.9 Wall thickness

Currently wall thickness is defined as the thickness along a radial spike from the endocardial or the epicardial center (depending on setting in the preferences. In the future I plan to also include the modified center line method.

Note that the centers are calculated for each timeframe separately.

Wall thickening is defined as the wall thickness in end-systole minus the wall thickness in end-diastole. Note that it is possible to manually or automatically select what timeframes that are diastole or systole respectively.

Fractional wall thickening is defined as:

$$WT_f = \frac{WT - WT_{ED}}{WT_{ED}} \tag{3}$$

Where $WT_f$ is fractional wall thickness and $WT$ is wall thickness and $WT_{ED}$ is wall thickness in end-diastole. In the bulls eye plot then fractional wall thickening is showed in end-systole.

## 27.10 Infarct size, extent and transmurality

Calculations of infarct sizes etc are based on 'counting' pixels, i.e. each pixel has a binary classification. There are two methods for regional analysis available, one are based where the percentage of the pixels that are inside the sector. The other method is based on radial spikes from the center (endo- or epicardial depending on setting in the preferences). The line between endocardium and epicardium is resampled in 50 steps and the percentage of infarcted pixels are counted.

Infarct extent is defined as the projected infarcted area on the endocardial surface [11].

$$I_{ext} = \sum_i \frac{T_i R_i}{R_i} \tag{4}$$

where $I_{ext}$ is the infarct extent, $T_i$ is the transmurality of sector $i$ and $R_i$ is the mean endocardial radius of sector $i$.

# 28 How to Reference the Software

To be permitted to use the software for research purposes you need to reference the usage of the software properly, for more details see Chapter 2. This is very important since it is necessary that we can prove to granting organisations that this project returns scientific output and has a significant impact to the scientific community.
A reference should encompass both the name and version of the software, and a reference to a suitable scientific publication about that function in Segment. It should also be indicated that the software is free for research purposes, and the address homepage of the software (`http://segment.heiberg.se`).

You should reference the software differently depending on what part of the software that have been used. This list is subject to change after submitted papers are accepted. *Always* check the homepage for the latest information regarding this issue. In doubt please do not hesitate to contact the author, or place the generic Segment reference [12].
Note that referencing the software is mandatory also for abstracts to scientific conferences. It shortage of space, reference the software as something like:

*... Images was analyzed using the freely available software Segment (`http://segment.heiberg.se`).*

In extreme shortage of space, such as conferences where the word limit is $<$ 250 words then reference may be omitted, and a reference should be included in the oral presentation or the poster.

- General usage of Segment should be reference [12]. This reference is the generic reference for the Segment project.
- Automated and manual delineation of the left ventricle on MRI images to get LV volume, ejection fraction, etc, should be referenced as [10] or [13], or possible [12].
- Automated quantification of infarct size and transmurality should be referenced as [5] or [4] depending on what mode have been used. If

weighted mode have been used to quantify infarct transmurality, then paper [14] should be used.

- Flow quantification should be referred to as [12].
- Strain analysis should be referred to as [15].
- Segmentation of the left ventricle in non gated SPECT images should be referenced to as [16].
- Segmentation of defect size of myocardial at risk from SPECT images should be referenced to as [17].
- Segmentation of myocardium at risk from T2 STIR imaging should be referred to as [18].
- Segmentation of myocardium at risk from cine delayed enhancement should be referenced to as [19].
- Measurement of endocardial extent should be referenced to as [11].
- Creating polar plots should be referred to as [20].

## 28.1 Examples of possible formulations

- *... left ventricular mass and ejection fraction was measured using Segment v1.8 R1172 (`http://segment.heiberg.se`) [13].*
- *... Infarct size were determined using Segment v1.8 R1172 (`http://segment.heiberg.se`) [5].*
- *... Image analysis was performed using the freely available software Segmentv1.8 R1172 (`http://segment.heiberg.se`) [12].*

# 29 Short Commands / Hot keys

This chapter describes the hot keys that can be used in the program. Note that in many places you can also bring up a pop-up menu by using the right mouse key to more easily access frequent menu items.

## 29.1 Hot keys

| | |
|---|---|
| `Left arrow` | Previous frame or pan left |
| `Right arrow` | Next frame or pan right |
| `Up arrow` | View next slice in basal direction |
| `Down arrow` | View next slice in apical direction |
| `Delete` | Delete segmentation in selected slices |
| `d` | Go to diastole |
| `f` | Copy segmentation forward |
| `h` | Hide contours and ROI's |
| `o` | Hide / Show viability overlay |
| `p` | Start to play movie |
| `r` | Refresh screen |
| `s` | Go to systole |
| `u` | Copy epicardium upwards and refine |
| `v` | Toggle view mode |
| `w` | Toggle image stack |
| `Space` | Toggle tool in toolbar menu (i.e switch from endo to epi tool). |
| `Ctrl-Arrows` | Same as single arrow keys but applies for all image stacks. |
| `Ctrl-0` | Reset GUI positions |
| `Ctrl-1` | One view |
| `Ctrl-2` | M-mode view |
| `Ctrl-3` | Montage view |
| `Ctrl-A` | Selects all slices |
| `Ctrl-B` | Bullseye plot |
| `Ctrl-D` | Copy segmentation or ROI downwards and refine |
| `Ctrl-E` | Segment epicardium |
| `Ctrl-F` | Propagate segmentation/ROI delineation forward |
| `Ctrl-G` | Auto delineate a vessel |

| | |
|---|---|
| `Ctrl-M` | Segment endocardium |
| `Ctrl-L` | Load segmentation |
| `Ctrl-O` | Load image data |
| `Ctrl-P` | Copy ROI to all timeframes |
| `Ctrl-Q` | Quit program |
| `Ctrl-R` | Refine endocardium or flow ROI |
| `Ctrl-S` | Save segmentation |
| `Ctrl-T` | Track tool for segmentation |
| `Ctrl-U` | Copy segmentation or ROI upwards and refine |
| `Ctrl-V` | Remove papillary muscle |
| `Ctrl-W` | Close current image stack |
| `Ctrl-Z` | Undo segmentation |
| `Ctrl-plus` | Zoom in |
| `Ctrl-minus` | Zoom out |
| `Alt-P` | Set current tool to pointer (i.e select) |
| `Shift-Left arrow` | Previous frame all image stacks |
| `Shift-Right arrow` | Next frame all image stack |
| `Shift-Up arrow` | View next slice in basal direction, synchronize all parallel image stacks |
| `Shift-Down arrow` | View next slice in apical direction, synchronize all parallel image stacks |
| `Shift-1` | View one image panel |
| `Shift-2` | View two image panels |
| `Shift-4` | View three image panels |
| `Shift-6` | View six image panels |
| `Shift-9` | View nine image panels |
| `Shift-A` | View all image stacks |
| `Shift-D` | Go to diastole all visible image stacks |
| `Shift-F` | Select Flow mode |
| `Shift-L` | Select LV mode |
| `Shift-S` | Go to systole all visible image stacks |
| `Shift-R` | Select RV mode |
| `Shift-V` | Select Viability mode |
| `Shift-Ctrl-W` | Close all image stacks |
| `Mouse wheel` | Scroll through slices in all image stacks |
| `Shift-Mouse wheel` | Scroll through frames in all image stacks |
| `Ctrl-Mouse wheel` | Scroll through visible thumbnails |
| `Alt-Mouse wheel` | Zoom |

# 30 Support

The commercial license of Segment includes technical support by email. It also includes simple feature request such as specialized output formats. Furthermore a commercial licensee will be given a significant weight on how a bug report is prioritized. Bugs reported by users of commercial license are usually fixed within 1-2 days. The support is provided by Medviso AB.

With this said, we encourage all users to come with questions and feedback, but we do not guarantee that we will have time to answer your questions.

## 30.1 Submit bug report

When submitting a bug report it is very important to describe how to reproduce the bug and to provide the log file for the session. In many cases it is also necessary to provide some files that can be used to analyse the problem. It may either be `.mat` files or DICOM files when the problem is loading data into Segment.

To submit a bug report, select the function Submit Bug Report. This will open the graphical user interface where you can describe the bug and attach log files and data such as `.mat` files or DICOM files. When all information is entered you press the Send support request and the description entered and the attached files are submitted to Medviso.

By changing the type you can also submit general questions or enhancement requests.

Hints to remember:

1. Even though the submitted files are encrypted your files should be anonymized. Anonymization of `.mat` files are available under either Image Tools menu or the Utilities menu. Anonymization of DICOM files are available under the Utilities menu.

2. Additional files to submit should be placed in a folder and the folder is then submitted.

3. Remember to name your files wisely, otherwise we will not be able to identify which file belongs to which support request.

4. Remember to mention the filename uploaded in your support question/request.

## 30.2 Data privacy policy

Medviso AB will strictly keep the data safe and **not** distribute it and any data or information from it (such as possible pulse-programming ideas, post-processing ideas, etc etc). Medviso will **not** utilize it for other purposes than debugging purposes or to answer the specific questions unless other is agreed upon. When the support case has been closed, then the data will be deleted. If you have questions, please contact `support@medviso.com` for further details.

## 30.3 General support issues

To get into contact with developers at Medviso AB, send email to `support@medviso.com`.

# 31 Segment user community

As a result of the growing interest in Segment and as a response of numerous requests Medviso AB has started to form a user community web place. This initiative will be enlarged significantly as the members of the community both requests more and also expands the community. It is worth noting that in the user survey spring 2010, out of 169 answers 147 answered that they would follow the user community, and 45 answered that they would follow it often.

A preliminary start page of the user community can be found on the following Facebook page `http://www.facebook.com/pages/Segment/119840021370285`.

It is the aim to be able to provide the following activities on the user community pages:

1. Participate in discussion forums. Currently forums for Developers discussion and tips and tricks, Feature requests, Segment and Mac.

2. Contribute and share own plug-ins. This feature is currently not available. If you have plug-ins that you want to share, please email them to `support@medviso.com` and we will manually upload the plug-in. Currently writing own plug-ins to Segment is documented in the Segment Technical Manual, and two plug-in examples are documented in Chapter **??**.

3. FAQ sections. Currently we are gathering FAQ in our support program. All (or almost all) support request will be made available in a searchable data base. Exceptions on when support requests are not included when the user request so in conjunction with classified projects.

Staff from Medviso AB will follow the user community page closely and monitor any incoming questions or uprising discussions.

If you have any ideas or suggestions on how we should improve the user community, please send us an email to `support@medviso.com`.

# 32 SPECT Analysis Module

The functions described in this chapter is off label use and for investigational use only.

The SPECT Analysis Module is work in progress and therefore only the automated segmentation of the left ventricle contour in non gated SPECT images and automatic segmentation of the perfusion defect region are currently freely available.

The SPECT analysis module can be used in both gated and non-gated image stacks. In gated image stacks segmentation of the left ventricle wall can be performed. In the non-gated image stacks also the perfusion defect region can be segmented. Analysis of gated images will be made freely available upon publication of these algorithms.

## 32.1 Visualization

In addition to the regular view of image stacks within Segment there are two visualization views specific for SPECT images. By using Plot 2D view under the SPECT menu a seperate graphical user interface is opened with three short-axis slices (one basal, one midventricular and one apical slice) and horizontal and vertical long-axis projections. The user interface is shown in Figure 44). In the left panels the stress image stack are shown and in the right panels the rest image stack. For Segment to be able to identify the rest and stress image stack, the `Image Type` has to be defined as Perfusion Stress and Perfusion Rest, respectively. For gated image stacks this visualization is time resolved. For gated image stacks with LV segmentation, the left ventricular blood volume is illustrated as a curve over time in the lower right panel in the interface.

A three dimensional view of the counts and scar within the myocardium is presented by using Plot 3D view under the SPECT menu. This will open a separate graphical user interface, shown in Figure 45.

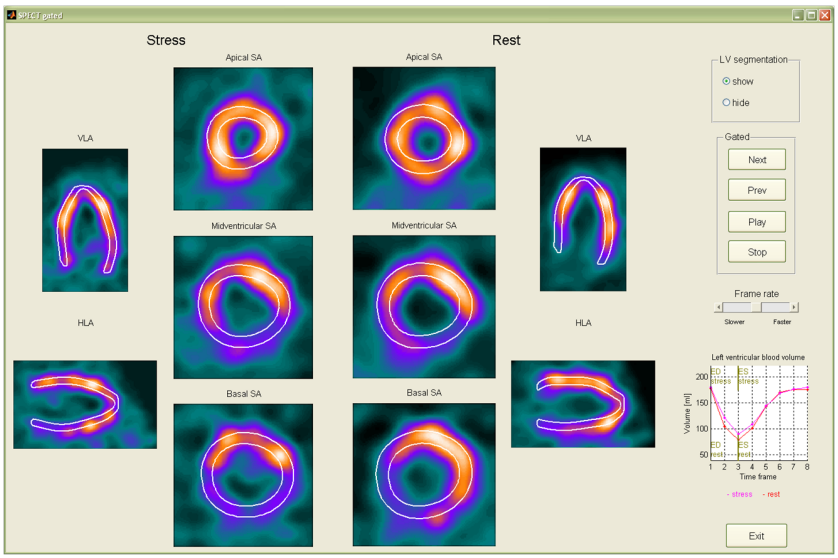



Figure 44: Graphical user interface of the 2 dimensional visualization for SPECT images.

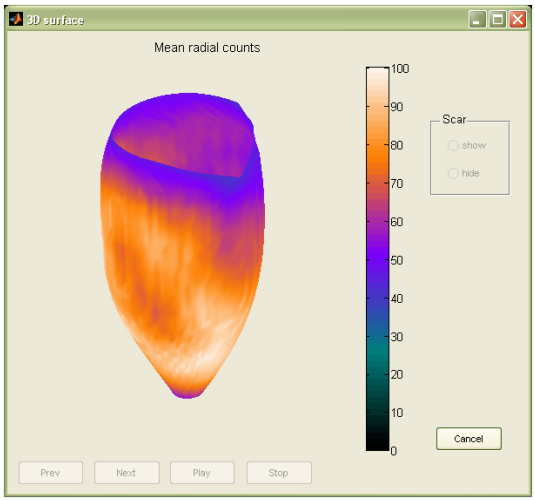



Figure 45: Graphical user interface of the 3 dimensional visualization for SPECT images.

## 32.2 Automatic segmentation of the left ventricle

The function Auto Delineate LV under the SPECT menu automatically segment the left ventricle in the current image stack. To use the function the image stack must fulfill the following requirements.

- The image stack need to be in short-axis projection.
- The "Number of points along the contour" must be greater then or equal to 50 (in the Preferences menu).
- The slices have to be in the order basal to apex when go through the slices from the top to the bottom. If this requirement is not fulfilled use the function Flip z (also Flip in x) under Flip & Rotate→Image tools.
- The septal part of the heart have to be in the left side of the image.

A segmented left ventricle is shown in Figure 46. The endocardial segmentation is illustrated as red lines and the epicardial segmentation as green lines.

### 32.2.1 Manual corrections

If the results from the automatically segmentation method is not good enough, the user can do manual corrections. This can be done in four ways:

- Crop the image stack. If there are extra-cardiac activity this can affect the segmentation.
- Manually select short-axis slices in the segmentation. This is done by select all slices for the segmentation by using the icon (find in the lower right panel in the main GUI).
- Manually point out the center point of the left ventricle. Use the icon (find in the lower right panel in the main GUI) and place two points in the middle of the left ventricle in two different image slices. The program then adjust a center point line through all slices by adjusting a straight line to these two center points. It is important that it is just two points because otherwise the segmentation algorithm ignores them and automatically select center point.
- Manually change the finished segmentation with the pen for endocardium segmentation and epicardium segmentation .

## 32.3 Automatic segmentation of the perfusion defect

To make an automatic segmentation of the perfusion defect in the segmented left ventricle use the function Auto Delineate Defect under the SPECT menu. The perfusion defect in the SPECT image are defined as a region with low intensity. The intensity limit that define the perfusion defect are set by the SPECT defect preferences. These preferences are described in the next section. An example of an outlined perfusion defect are shown in Figure 46. The red and the green line in the figure are the left ventricle segmentation and the yellow line the outlined perfusion defect.

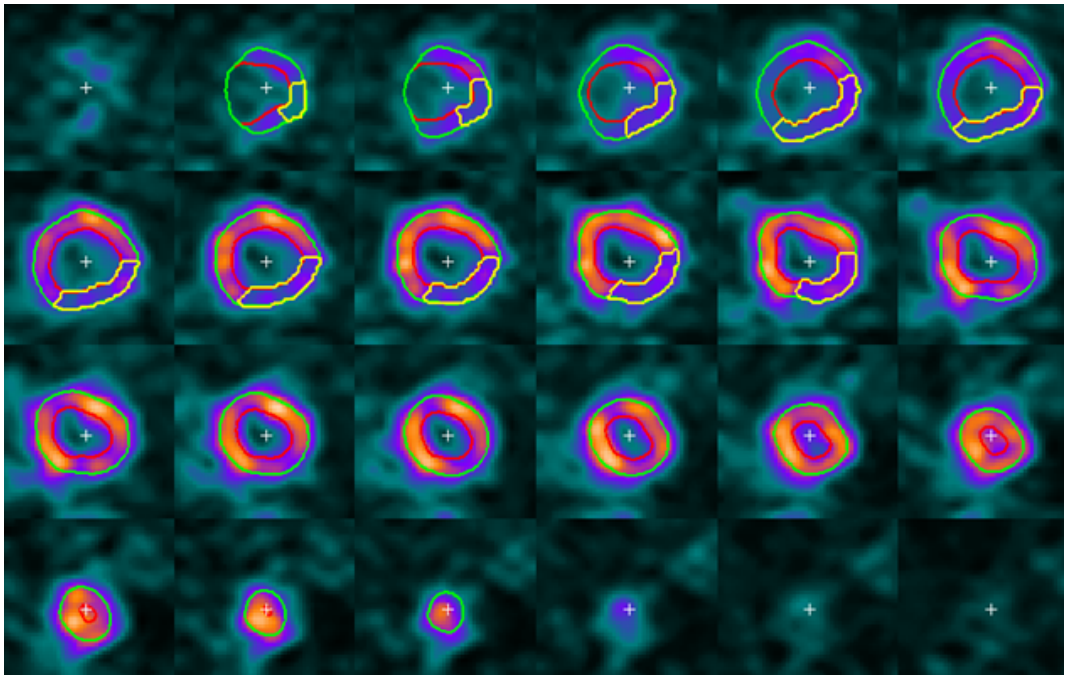


Figure 46: An example of a segmented left ventricle with the defect region outlined. The red line is the endocardium, the green line the epicardium and the yellow line the perfusion defect.

### 32.3.1 Set preferences

The SPECT defect preferences are set by the function SPECT preferences under the SPECT menu. The preferences are set for each image stack which

make it possibly to have different preferences for different image stacks.

The SPECT defect preferences GUI is shown in Figure 47. The choice made in the upper panel determine the region for which the count calculations are done in. The two selections are Image and ROI (the default value). The Image selection include all pixels in the image in the defect calculation while the ROI selection only include the pixels within the roi (here the left ventricular wall) in the calculations. The "Count Maximum" number is defining the percentile (the default value is 100%). The "Threshold" number is determined the percent of Count Maximum which defined a defect (the default value is 55%). All pixels with a count lower than this value are included in the defect region. The "Minimum volume" number determined the smallest volume for a defect (the default value is 10%). The number are percent of pixels in the image or in the ROI. All defects with a volume smaller than this number are excluded from the defect segmentation. The two selection for the subdivision of the LV used in the a priori model are the default model (based on normal coronary artery perfusion territories) and the standard 17-segment model. The choice in the lowest panel determine if the a priori model of the coronary distribution should be used in the defect segmentation or not.

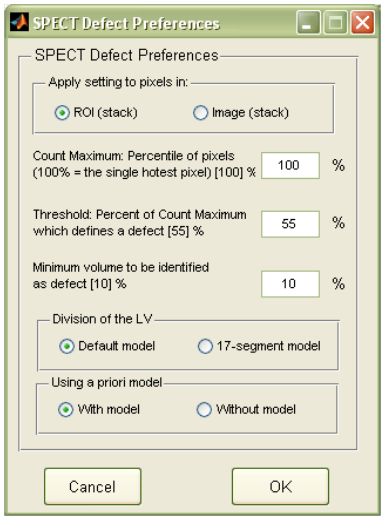



Figure 47: The SPECT defect preferences GUI.

### 32.3.2 Reset defect

To reset the perfusion defect calculation use the function Reset Defect under the SPECT menu. This function both reset the defect segmentation and the SPECT defect preferences for the current image stack.

# 33 CT Module

The functions described in this chapter is off label use and for investigational use only.

Currently we are working on a CT Module that will be useful for automated segmentation and image analysis of CT images. Currently this functionality is only available upon request.

In the module functionality for automatic segmentation of pericardial sac (whole heart CT), automatic identification of the coronary ostia, and automated bone segmentation. The automated segmentation of the pericardial sac will be highly useful for visualization of the coronary arteries in conjunction with the volume rendering module that is work in progress.

Please contact Medviso AB to get a demo of these features.

# 34 Strain Analysis Module

The functions described in this chapter is off label use and for investigational use only.

The strain analysis module uses velocity encoded MR images to calculate myocardial strain. The module have been written by Helen Soneson as her Master thesis work [21], and resides on the work by Erik Bergvall for strain calculations and myocardial tracking [22]. This module is not available yet to researchers since it is under development and will be released as soon as the underlying method is properly published. Preliminary results about the method was presented at SCMR 2008 [15],[23].

Strain calculations require velocity encoded MR images with two velocity components. An example of such an image stack are shown in Figure 48. The leftmost panel is the magnitude image stack the two rightmost are the velocity image stacks.

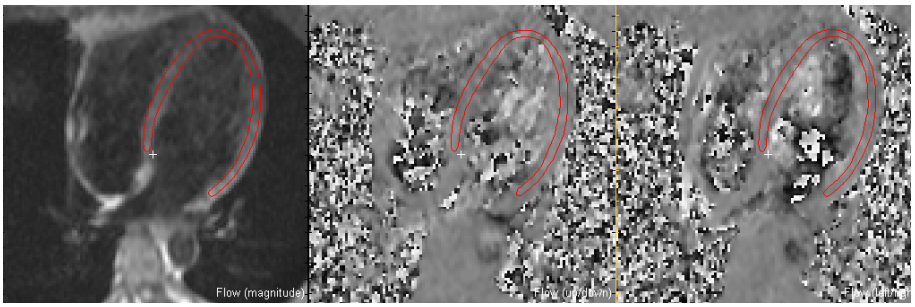



Figure 48: Example of a velocity encoded magnitude image stack and two directional velocity encoded image stacks.

## 34.1 Long-axis

Before starting strain calculation the myocardium of the left ventricle need to be manually outlined in end-diastole. One method to do this is to use the endocardium tool directly in the velocity encoded image stack. One

tip before outline the myocardium in a long-axis image is to first set the "Number of points along the contour" in Preferences under the Preferences menu to 300. This make it easier to do small changes in the segmentation. The other method is to segment the myocardium in the anatomical (balanced or SSFP) image stack and then exported it to the velocity encoded image stack. The exportation is done with the function Import Segmentation from SSFP under the Strain menu. Before calculating strain the image type have to be set to either "Strain 2CH TFE" or "Strain 2CH FFE" (and similar for 3CH and 4CH). This is done either upon loading or by right clicking on the corresponding thumbnail images and select Set Image Type.

### 34.1.1 Strain calculation

The strain in a long-axis velocity encoded image stack is calculated by using the function Calc/View under the Strain menu. Note that you need to manually outline the myocardium in end-diastole first. The function calculates segmentation and strain in all time frames. It also opens a new graphical user interface that make it possible to analyse/visualize strain in the image. An example of such a GUI can be seen in Figure 49.

To select which strain or displacement parameter to analyse, mark one of the parameters in the listbox in the figure. The 12 alternatives are:

- P1, the largest eigenvector to the strain tensor
- P2, the smallest eigenvector to the strain tensor
- Frobenius, the Frobenius norm of the strain tensor
- Ex, strain in x-direction in the image
- Ey, strain in y-direction in the image
- Exy, shear strain in the x-y coordinate system
- Srad, radial strain
- Slong, longitudinal strain
- Sshear, shear strain in the radial-longitudinal coordinate system
- Displacement, the total displacement
- Disprad, radial displacement
- Displong, longitudinal displacement

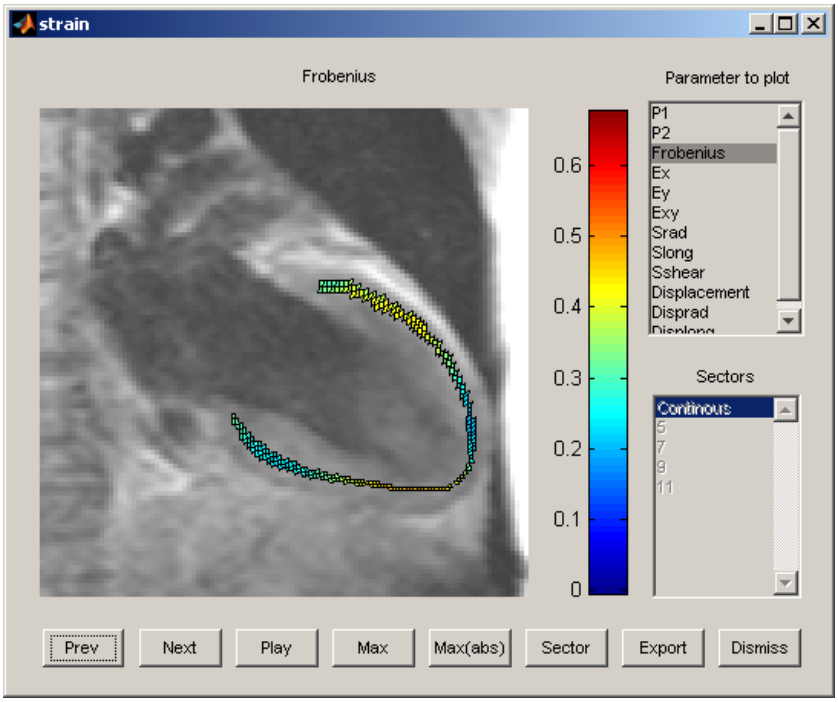



Figure 49: Example of the strain GUI.

To see how strain changes over time there are three buttons in the figure to use. Prev that step one time frame backward in the heart cycle. Next that step one time frame forward in the heart cycle and Play plays a movie of strain over the whole heart cycle. The buttons Max and Max(abs) produce a figure of maximal strain (and maximal strain in absolute values) in each pixel over time. For an example se Figure 50.

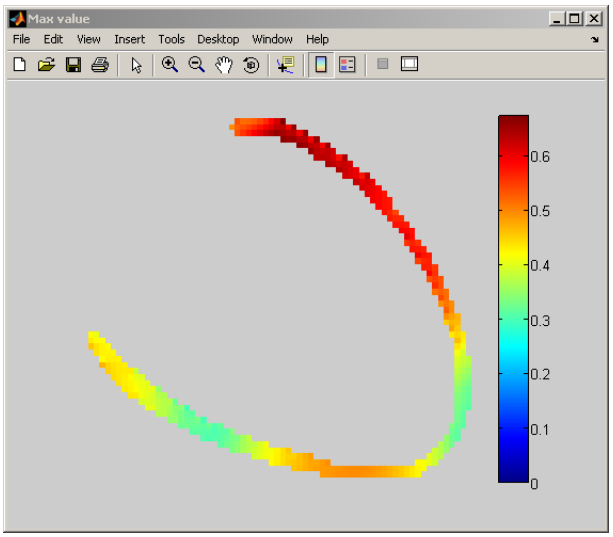



Figure 50: Example of the maximal strain value figure.

The Export button export strain values to a clipboard. These values are only given section-wise, and the values in each sector corresponds to the mean value of the pixels in the sector. The sectors are divided according to American Heart Associations 17-segments model. The button Sector illustrate the section division.

The graphical user interface can also be open by selecting View under the Strain menu. This will open the interface without first recalculate strain.

### 34.1.2 Corrections of the segmentation

To make manual corrections in the calculated segmentation select Manual Corrections under the Strain menu. This open a new window, se Figure 51 for an example, where you can correct the segmentation in all time frames

except the first one.

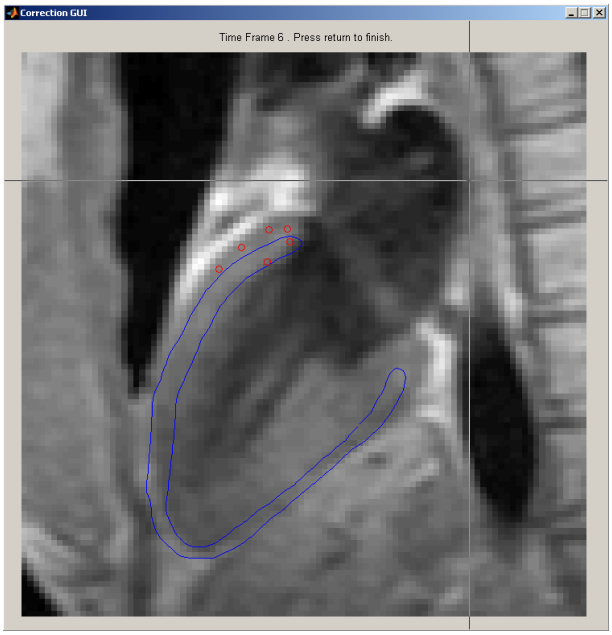



Figure 51: Example of the correction figure.

To correct the segmentation in the image use the left mouse button. This will result in a red ring for which the segmentation curve will be adjusted to. To erase a correction point use the right mouse button. Step between the time frames using the arrow keys on your keyboard. When you are satisfied with the segmentation in all time frames push the return keyboard button. Then choose Yes in the confirm figure to make a new strain calculation and No to cancel all correction points out.

Since there can not be corrections done in the first time frame, the original (before the corrections) segmentation can always be recalculated by select Calc/View under the Strain menu. This will on the other hand erase all correction points. To avoid this when analyzing strain with made corrections use View under the Strain menu instead of Calc/View to open the graphical user interface (Figure 49).

### 34.1.3 Strain analysis

One method to evaluate the strain calculation is to export the segmentation from the velocity encoded image stack to the SSFP image stack after the strain calculation is done. This is done with the function Export Segmentation to SSFP Image under the Strain menu. The motion of the myocardium can then be compared to the myocardial movement in the SSFP image stack. It should be noticed that the two images (SSPF and velocity encoded) are not acquired during the same heart beat which can result in differences in position of the myocardium.

With strain calculated in the current velocity encoded image stack it is possible to produce a graph over time for strain by the function Graph over time under the Strain menu.

In a file that consist of velocity encoded image stacks with calculated strain in all the three long-axis views it is possibly, by the function Polar plot under the Strain menu, to produce a polar plot of strain. To use the function the septal/anterior part in the long-axis have to be pointed out by the tool . Se Figure 52 for an example of a polar plot of strain.

The strain values in the current heart can be compared to both a normal model or another file containing long-axis velocity encoded image stacks. To compare strain with the normal model use the function Compare to Normal Model under the Strain menu. Then select either pixel-wise or section-wise analysis and which parameter to analyse. For the section-wise comparison it is necessary that the current file consists of calculated strain in all three long-axis views and that the septal/anterior part of the long-axis is pointed out. To point out the septal/anterior part use the tool . To compare strain in the current heart with strain values from another file use the function Compare to Another File under the Strain menu. The section-wise selection require strain values in all three long-axis velocity encoded image stacks and the septal/anterior part pointed out in both hearts. The pixel-wise analysis only require strain in one long-axis velocity encoded image stack.

The function Calc/Save Multiple .mat Files under the Strain menu calculate strain in all `.mat` files in the selected folder. To calculate strain the function required a segmentation in the first time frame in the velocity encoded image

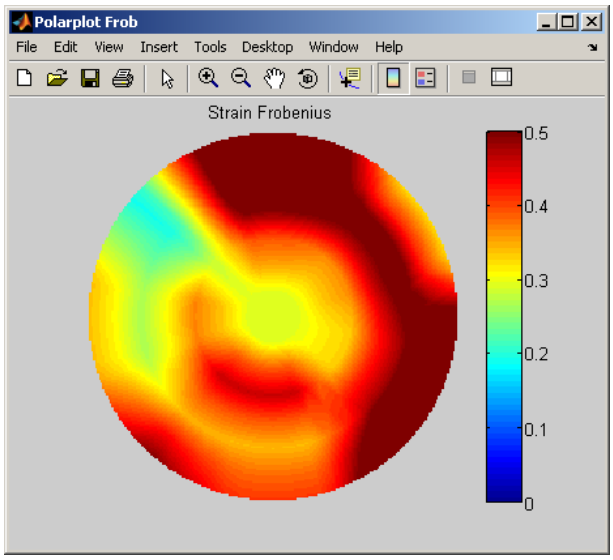



Figure 52: Example of a polar plot of strain.

stacks. The files are then saved with strain calculated in all long-axis velocity encoded image stacks. The function Export Strain Multiple .mat Files under the Strain menu exports strain values to clipboard in all `.mat` files in the selected folder.

### 34.1.4 Late enhancement image

To see the infarcted region outlined in the strain image use the function Infarction Mapping under the Strain menu. This function result in a figure that illustrate pixel-wise strain from the velocity encoded image stack and the outlined infarcted region. The infarcted region are received from the scar region in the late enhancement image stack. The function requires that strain is already calculated in the velocity encoded image stack. It also needs a myocardial segmentation, an infarction segmentation and image type set to "Late enhancement 2CH" or 3CH or 4CH in the late enhancement image.

The segmentation in the late enhancement image stack can be done by manually using the or by the function Export Segmentation to Infarct Image under the Strain menu. This function takes the segmentation in diastasis in the velocity encoded image stack and copies it to the late enhancement

image stack.

## 34.2 Calculating Short-axis

To calculate strain in a short-axis image stack the image type have to be set to either "Strain short-axis Basal", "Strain short-axis Mid" or "Strain short-axis Apical". The two right ventricular insertion points also have to be pointed out by the tool . To calculate strain use the function Calc/View under Strain→Short axis. This result in a figure similar to Figure 49. Note that this functionality is still experimental.

# 35 Image Fusion Module

The functions described in this chapter is off label use and for investigational use only.

This module is not available yet to researchers since it is under development and will be released as soon as some application papers have been properly published. The module has been written by Helen Soneson.

The image fusion tool is used to compare and fuse one anatomical and one functional image stack. Currently the tool is restricted to rigid body translation and rotation.

An example of the fusion GUI is shown Figure 53. The leftmost panel is the anatomical image stack, the middle the functional image stack and the rightmost the fusion image stack.

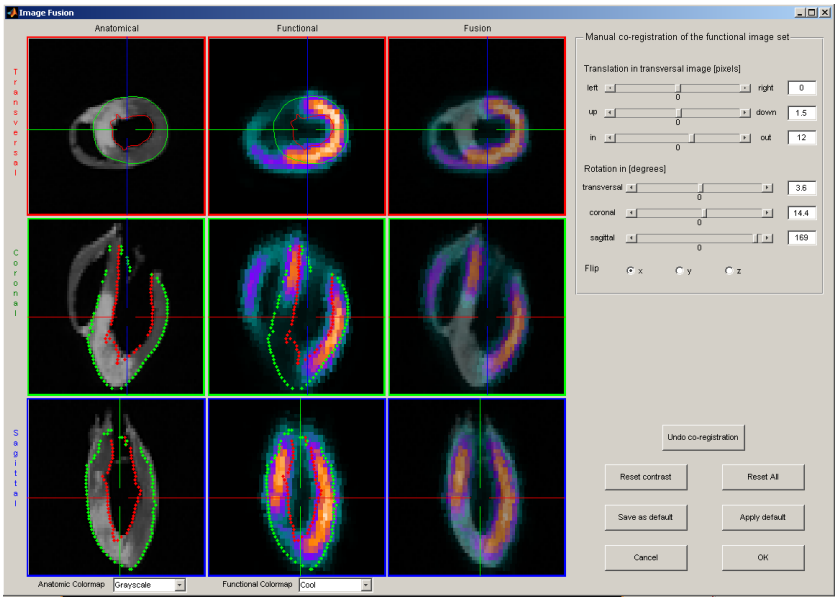



Figure 53: Example of the image fusion GUI.

To start the fusion tool select Fusion of Two Image Stacks under the Fusion

menu. You will then be prompted for which anatomical and functional image stacks to fuse. You select by entering a number that are the same as the thumbnail order (from left) in the main Segment GUI. If the anatomical image stack contains a segmentation this will be shown both in the anatomical and the functional image stack.

Below each image stack the user can manually select color map. The two selections are gray and cool and can be different for the two image stacks. To change the transparency in the fusion image stack hold the right mouse button down and move up or down. In the anatomical and functional image stack the right mouse button will change the brightness (up/down) and contrast (right/left). Click on the left mouse button define the current slice in the image stack. Same slices are always shown in anatomical and functional image stack. The arrow buttons on the desktop can then be used to step in the slices in the last clicked image. If the last click was in one of the co-registration sliders the arrow key buttons will change the position of the slider.

The manually co-registration of the functional image stack is done by changing the parameters in the right box in the GUI. The three sliders and editboxes on the top translate the image stack. The sliders and editboxes in the middle make a rotation in the image stack. The three radiobuttons below the sliders flip the image stack in x- y- and z-direction, respectively.

The Undo co-registration button undoes the last translation or rotation. It also undo the Reset all button. This button reset both co-registrations, colormaps, current slices, contrast and brightness in all image stack to the start values. The Reset contrast button only reset contrast and brightness in the anatomical and functional image stack, and the transparently in the fusional image stack to initial values.

If you need to fuse many data-sets with approximately the same parameter settings, the default buttons can be helpful. The Save as default button saves the current translation, rotation, flip and colormap choices. These settings are then available to use on another data-set. The settings are applied to the image stack by using the button Apply default.

When you are satisfied with the fusion use the Ok button. This results in a new image stack with image type "Fused" and contains the functional images stack, with the anatomical image stack size, and the segmentation from the anatomical image stack. Example of such an image stack are shown in Figure 54. The parameter settings are also saved and the fusion GUI with the old parameter choices can be open again by select Fusion of Two Image Stacks under the Fusion menu when having an image with image type "Fused" selected. When an image stack with another type than "Fused" is selected, a new fusion GUI always open. Pushing the Ok button in the fusion GUI always result in a new fused image stack.

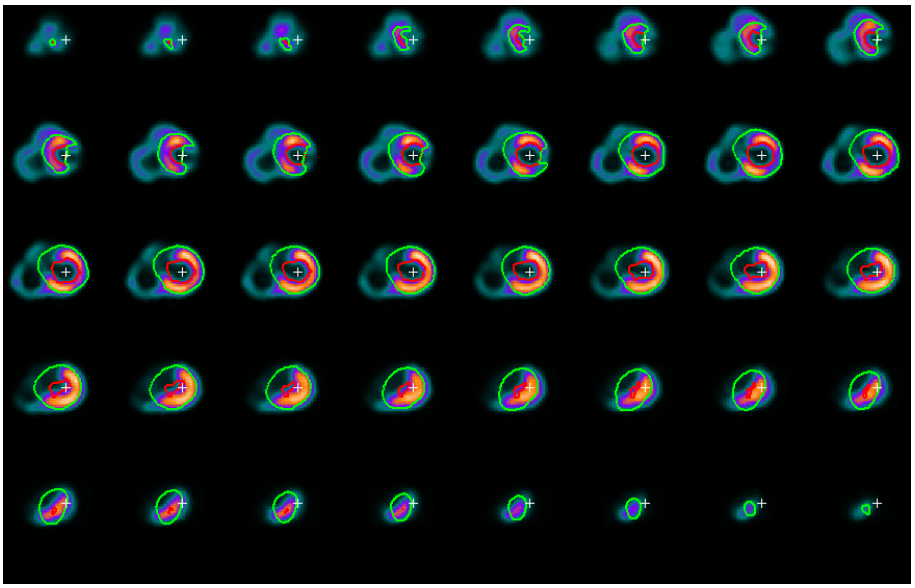


Figure 54: Example of a fused image stack.

# 36 Native Bruker Reader Module

The functions described in this chapter is off label use and for investigational use only.

This module to load native Bruker files is not available in the research only version of Segment. To use this module you need a support contract with Medviso AB. The structure (files and directory) of the Bruker Paravision file format is given in the Imaging Wiki:

`http://imaging.mrc-cbu.cam.ac.uk/imaging/FormatBruker`

The reader is available under the File menu. The file loader GUI is shown in Figure 55.

The first step is to select the subject file. This file is usually called just `subject` or `subject.txt`. Then all available subject info is shown in the top left panel. A list of available studies are shown in the lower left panel. When selecting on study the image series (usually only one) are displayed. The Load will load the selected studies/series. To load many studies into one image stack, just select more studies in the lower left panel. Note that when loading many studies into one image stack each study needs to contain only one image serie.

The checkbox ☒ Flip time/slice is used to flip between slices and timeframes. This may in some circumstances be needed, since there seems to be a bug in the fileformat specifications for some versions of the Paravision system. The button Dismiss will close the file loader. The button Clear will clear the current subject to allow you to select another subject.

The following limitations apply to the Bruker reader:

- The reader is still experimental and all paravision features may not be implemented. If you are experience problems with the Bruker reader, please report them.

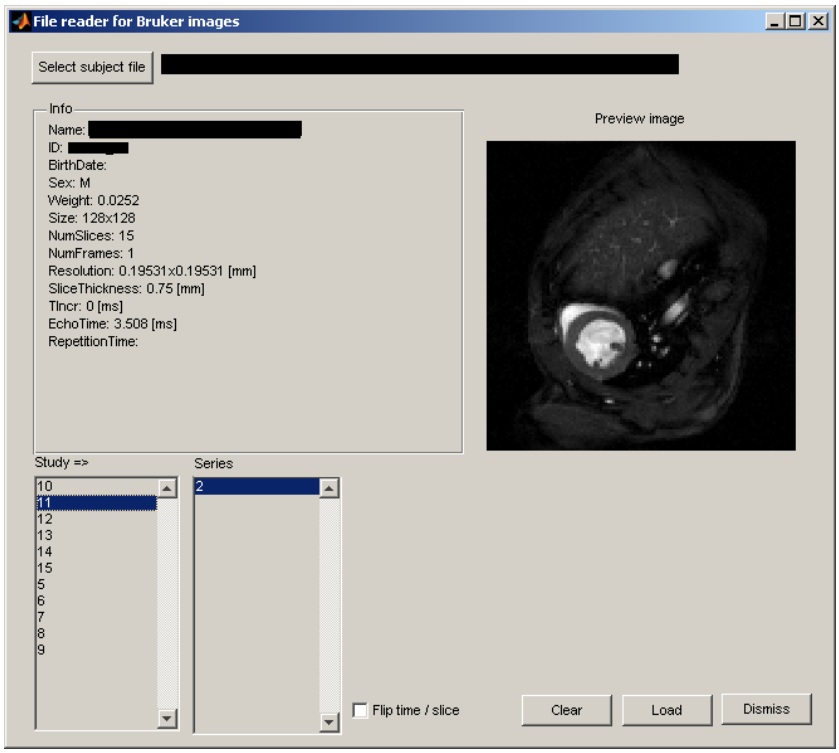



Figure 55: File GUI for loading bruker images.

- The reader does currently not read 3D coordinates, and thus the plane intersection features in Segment will not work.

# 37 Patient Database Module

The Patient Database allows you to easily keep track of your patients and effecient and simple loading of image data into Segment.

Segment uses the well validated OFFIS DICOM Toolkit DCMTK (C) 1993-2006, OFFIS e.V to do the low level image transfer operations. Most DICOM workstations and PACS requieres that all clients connecting to the server is added to a security list with `Calling_AE` and IP number. Therefore, you will need to contact the system administrators before you can use this functionality. Often there might be a firewall on your computer that needs to be configured to allow the communication. Ask your local system administrator or segment support for help. Setting Segments AE-title and port is done in the preferences, see Chapter 25 for details.

The aim of the patient database is give the user an overview of available patient studies that are stored on the workstation and to facilitate loading of data. It is not designed to replace a hospital PACS for long time image storage. If so desired you should complement Segment by purchasing a commercially available PACS or freely available such as Conquest PACS. For further help with designing an appropriate system for managing large patient image archives, please contact Medviso AB.

The graphical user interface of the patient database is shown in Figure 56. In the listbox all available studies which fullfilles the searchcriteria are shown. In the listbox information on patient name and ID, imaging modality, study date and file format, either DICOM or Segment is given.

## 37.1 Search a study

Studies can be search for by using the different criteria, patient name, patient id, comment, imaging modality and study date. Search starts immediately when starting to type one of the criteria an the studies which fulfills all searchcriteria is shown in the listbox.
To search for a study by patient name start typing and the letters will automatically be placed in the edit box `Name` and the search will start. The

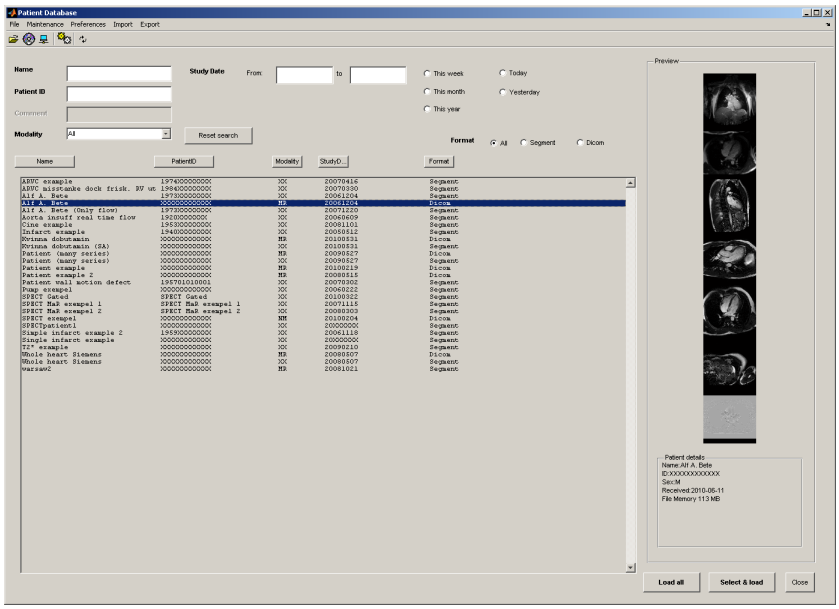



Figure 56: Graphical user interface of the patient database.

letters typed in the edit box will be searched for at any place in the patient name, that is to say if you type in an 'a' it will match with both 'anne' and 'julia'. Wildcards such as '*' should never be inserted since the algorithm automatically uses such an approach.

If a number is typed instead of letters it will automatically be inserted in the `Patient ID` edit box. The search for patient id works in the same way as the search for patient name.

The search for `Comment` is not yet available but will be a feature where you can search for a comment on the study after it has been saved in the internal Segment format.

To only find studies of a certain imaging modality change in the pop up menu `Modality` from `All` to the imaging modality of your choice.

Searching for a study by the date of the date can be done in two ways, by searching for studies within a week, month or year by using the radiobuttons

`This week`, `This month` or `This year` or by editing `Study date` in the edit boxes `From:` and `to`. To start typing in either of the edit boxes first click in the box. When starting to type the search will immediately start. When typing '2' in the from box all studies after '20000101' which fullfils the other searchcriterias such as name and patient id will be shown in the listbox. When the whole date has been typed in both the from and to boxes the search will result in only those studies performed between those two dates. To be able to change in the patient id or name edit boxes again a mouse click in the edit box must be performed first.

The studies can also be searched for by matching the `Format` of the file, either Dicom or Segment. This is done by changing the format radiobutton from `All` to either `Segment` or `Dicom`.

When deleting in a search criteria a thorough search will be done to show all studies that match the searchcriteria still present. All search criteria can also be deleted by using the button Reset Search

## 37.2 Sort studies

The studies in the list box can be sorted by the different criterias by pushing the buttons Name, Patient ID, Modality, Study Date or Comment.

## 37.3 Load a study

To load a study select it in the list box and push either the button Load all or Select & Load. The button Select & Load is only available if the format of the study is Dicom and it allows you to choose which series to load in the graphical Dicom selector, described in 9.1.6.

## 37.4 Technical details

The patient database resides on a simple directory structure and an index file to keep track of the files. In the folder `DICOM`, raw unprocessed DICOM images are stored. In the folder `Analyzed` processed files with contours, measurements and annotations are stored. The location where the patient database is stored can be adjusted in Segment preferences. When moving

the database to a new location, then the index file need to be regenerated. The index file can be regenerated by using maintenance functionality . Do absolutely not attempt to manually insert DICOM files into this file structure. Instead use the importing tools provided under the Tool menu.

## 37.5 Maintenance of the patient database

Currently there is no automation to delete old studies, this has to be scheduled manually. The graphical user interface for database maintenance is shown in Figure 57.

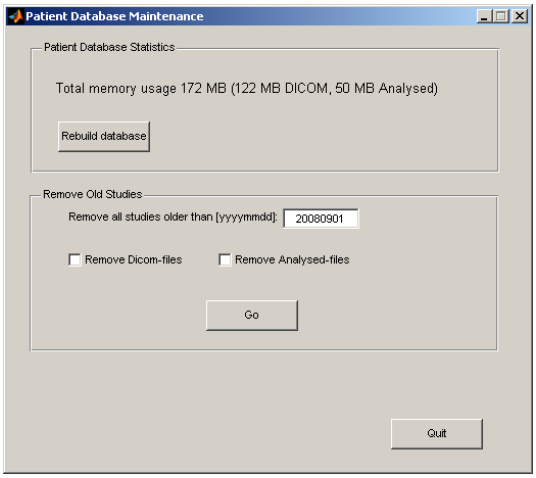



Figure 57: Maintenance graphical user interface.

## 37.6 Import studies

Studies can be imported to the patientdatabase in three different ways, from CD, from PACS and from network/disc. The import function can be found under the menu Import. When chosing to import from CD it is possible to restrict the import to be only dicom format otherwise both dicom and segment format files will be imported. When importing from PACS the PACS connection will be started and how to search for and retrieve files from the PACS is further described in Chapter 39. Importing from network

or disc is done by choosing from which location to import files and then choosing which format to import.

## 37.7 Export studies

It is also possible to export files in dicom format from the patientdatabase. This can be done by either selecting multiple files, exporting the one file selected in the listbox or by exporting all dicom files. If you want to select multiple files to export you add files to an exportlist by selecting the file in the listbox and then going to the menu Export and selecting `Add DICOM files to exportlist`. This procedure can be repeated until you have added all the files that you want to export. The files selected can be shown by selecting `Show exportlist` in the Export menu. When satisfied with the export list select `Export DICOM files to PACS` in the Export menu. This pops up an GUI in which you choose either to export selected files. To export the files the correct PACS system must be selected from the drop down menu.

# 38 Segment DICOM Server Module

The the Segment DICOM server is a separate program and by having this running on a computer it is possible to send DICOM files directly from a Scanner or DICOM complient workstation.

Segment uses the well validated OFFIS DICOM Toolkit DCMTK (C) 1993-2006, OFFIS e.V to do the low level image transfer operations. Most DICOM workstations and PACS requieres that all clients connecting to the server is added to a security list with `Calling_AE` and IP number. Therefore, you will need to contact the system administrators before you can use this functionality. Often there might be a firewall on your computer that needs to be configured to allow the communication. Ask your local system administrator or segment support for help. Setting Segments AE-title and port is done in the preferences, see Chapter 25 for details.

## 38.1 Segment DICOM Server

In order to make it possible to retreive images from imaging devices and other DICOM workstations a separate server software needs to be installed and running on the computer. This software is called Segment DICOM Server. This software is started by clicking on `segmentserver.exe` in the Segment folder. For help how to set up the server to automatically start when the computer is started, please contact `support@medviso.com`.

It is not possible to have the Segment DICOM Server Module without the Patient Databse Module described in Chapter 37. A typical overview of the dataflow when using the Patient Database and DICOM Communication Module is shown in Figure 58.

The graphical user interface of the Segment DICOM Server is simple and shown in Figure 59. A green box indicates that the server is idle and are waiting for requests. An orange box indicates that the server is processing

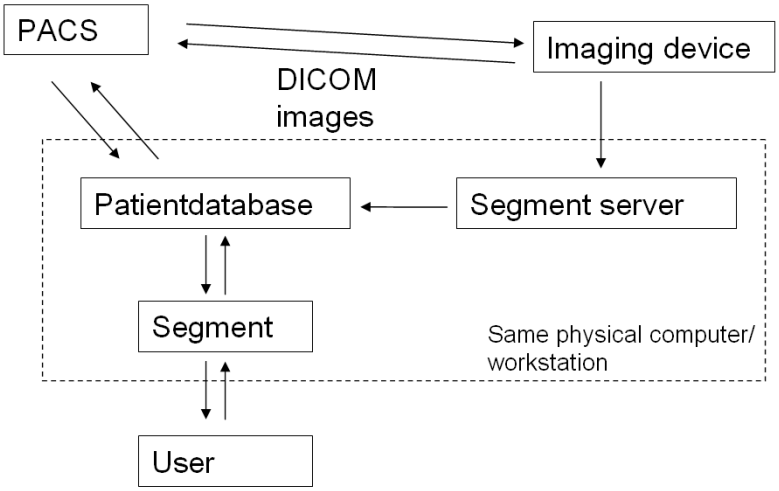



Figure 58: Example of datatransfer structure. The dashed box represent the same physical computer equiped with both the software Segment and the Segment DICOM Server installed.

incomming connection(s). To get the total number of files received, press the Stats. button.

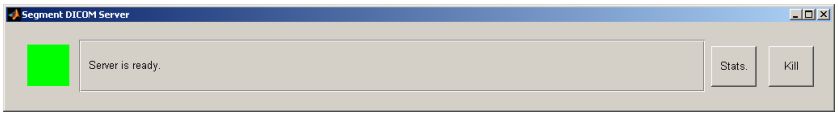



Figure 59: Example of the Segment DICOM Server GUI. A green box indicates that the server is idle and are waiting for requests. An orange box indicates that the server is processing incomming connection.

## 38.2 Troubelshooting

In case there are problem with the Segment DICOM Server Module, all error messages are stored to a `.log` file. Please submit these `.log` files when contacting the Segment support. For further details on how to submit bug reports or .log files, please see Chapter 30.

# 39 PACS Connection Module

The PACS connection GUI is started by the clicking on . The graphical user interface for the PACS connection functionality is shown in Figure 60. In the upper left corner of the GUI you can select what PACS to connect to. You need to add data for your PACS server. Do this is done in the Segment preferences under the Preferences menu, and then by clicking on Advanced System and DICOM Settings.

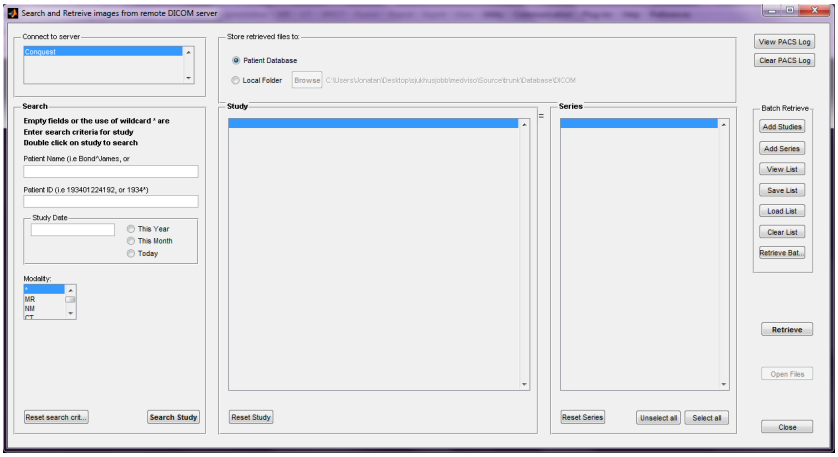



Figure 60: Screen-shot of the PACS search and retreival GUI.

## 39.1 Setting up

To set up which PACS or DICOM workstation to connect to, use the top left panel in the GUI. You need to know AE-title of the system to connect to (Called AE), Peer IP-address, and your AE-title (this should almost always be the same as the one set in the preferences). Finally Port is any valid port used to transfer the images.

## 39.2 Searching for studies

The most common approach is to search for a desired patient. You can enter either patientname or patient ID. The wildcard * is allowed. The

wildcard * may represents zero, one or more letters. The patient first name is followed by a ∧ and the surname. For instance the search string `bo*` will find `Bond∧James`. Note that there is no difference made on versal or capital letters. The search string `*Ja` will also find `Bond∧James` since once at least one wildcard is entered, then an implicit wildcard is added on the end.
For Swedish users the PatientID system allows to search on patients born a specific year. Entering `*Bert` as patientname and `1934*` as Patient ID will find patients who are born in 1934 and with names such as `Bert` or `Berta`. Note that it will also find `Bertilsson∧Arne` since the wildcard * may represent no or more letters.

Studies can also be searched for by editing the criterias study date and imaging modality. Study date can be entered either as a particular date or by using the radiobuttons `This Year`, `This month` oc `Today`.

Double click on the desired study and the available image series will be shown. Select the desired image series with the shift or control keys. There is also a Select all pushbutton to select all image series.

## 39.3 Retrieving files

When you have selected your desired image series it is time to retrieve the data. This is done by the pushbutton Retrieve. Before starting the retrieve operation ensure that the retrieved images are stored to the desired location. This can be adjusted in the GUI panel termed Store retrieved files to:.

The the images are stored in sorted subfolders. The first folder level is the patient name, i.e `Bond∧ James`. The second folder level is the study data, i.e `20060821`. The next folder level is the the series and are named as `Seriexxxx` where `xxxx` are a serial series number.

After retriving the files you can directly start the file loader with the pushbutton Open files. In the near future it will also be possible to do batch retrieval.

## 39.4 Batch downloading

It is possible to add studies and series to a batchdownload session. Start by searching for the desired patient. To add entire studies to the batch download

list select the desired studie(s) and press Add studies. To add specified image series, select the image series and press Add series. Note that you can select studies and series from several patients at the same time. To view what patients there are in the batch list press View list. It is possible to save the batchlist to a file for future use. To start the batch download retreival press Retreive batch. When retreiving a batch a waitbar is displayed with the number of series done and total number of files. The batch download takes to one series at a time. Some other commercial systems attempts to take several image stacks at the same time. By using so it might be possible for one client to use more band robots if the data have been swapped out to tapes. However, in our experience this leads to more instable systems.

## 39.5 Troubleshooting

The two most common problems are the firewall on the computer where Segment is run and denial from the PACS server. To facilitate debugging logging options are provided. There are two checkboxes that control the level of debug information stored. Note that only the latest search operation is stored. The log is viewed by the pushbutton View log. Another common problem is that when it works to search patients and when the image retreival does not work. The most probable cause is then security settings. Many PACS system are setup so that all clients may search images, but only selected clients are allowed to retreive images.

# 40 Communication Module

The functions described in this chapter is off label use and for investigational use only.

To facilitate communication and research cooperation a communication module have been included in Segment. Currently Medviso AB are aware of two multi center studies using Segment. The advantage of using this built-in communication module is that it enables encrypted transfering of files and there is no need to transfer passwords and usernames back and fourth.

The principle is that you need to have acess to an ftp site where your files resides that you want to send to your collaborators. An overview of the communication principle is shown in Figure 61. Upon specific request international multi center studies may be hosted by Medviso AB. Please contact `support@medviso.com` for further details.

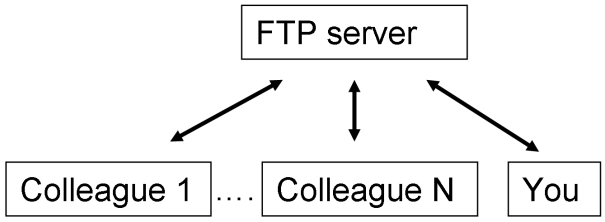



Figure 61: Overview of the communication process. All files are transfered to a remote FTP server.

## 40.1 Start a new collaboration

When you are about to start a new collaboration in which you want to be able to send files or retrieve files from, then the first step is to create a site key. A site key is a file that contains all necessary information that Segment needs in order to know how to submit or receive files. To create a

site key, use the Create New Site Key. The user interface to create a site key is shown in Figure 62. The first field `SiteName` should contain a descripte name of the site/collaboration. The field `HostName` should be the ftp adress to the site. The field `UserName` is the user name of the ftp account. The field `Password` is the password to the ftp site. Note that the site key store the password encrypted and the password will never be revealed to any user after it is typed in. The field `FolderName` is the sub directory of the ftp server in which the files are stored. You may use sub-sub folders and separate them with /, but it is not recommended. If required by the server you may have to start the folder name with /, but that is not the default behaviour of FTP servers. The field `SiteAdminEmail` should be the email adress to the person responsible for this communication profile or the ftp server administrator. In most cases it is strongly suggested that you type your own email adress in here rather than the server administrator. The field `HelpURL` is an URL to a help page if such is available. This field may be left blank if no such help URL exists.

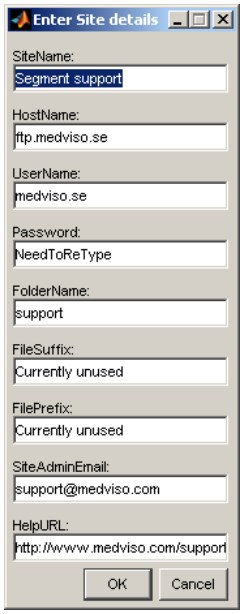



Figure 62: GUI for creation of a new site key.

When you have pressed OK, then you are prompted to give the site key a

filename.

## 40.2 Installing site keys

Simply store the site key you have created or recieved from a collegue in the same folder as where Segment is installed. The next step is to send this site key to your colleague(s). Ideally site keys should be transferred securely to the recipient(s) since it contains encrypted passwords and a long password used for file encryption. In most cases however, sending this site key as an email attachment is sufficient since all data is encrypted.

Please note that it is possible to use the same physical ftp server for several collaborations, just remember to give them different folder names when creating the site keys.

## 40.3 Share files using existing site key

The main GUI for the communication module is shown in Figure 63. Start by selecting the intended site to use send or receive files from. This done in the top right panel of the user interface. The main portion of the communication module user interface are two symmetrical panels showing files in the local folder (i.e your computer) and the remote folder (i.e on the server). The left panel shows your local files, and the right panel shows the remote files. Please note that it is only possible to transfer files, not complete directory structures. This is to ensure that users only can see the folder that is set in the site key. If you need to transfer entire folder structures, please zip the folder into one file. To upload files, select the files to upload in the left panel and hit Upload Files. To download files select which files to download at the remote site and select Download Files. Note that when you have encryption toggled, then the files are uploaded and stored encrypted on the FTP server and the string `_encrypted` is added as a suffix to the filename to show that the file is encrypted. When the file is downloaded from the server the file is automatically decrypted and the file suffix is removed.

It is possible to change the local folder directory by using Select Local Folder. Default local folder is otherwise Segment data folder set in the preferences. The button Refresh refreshes the file lists on both the local folder and the remote folder.

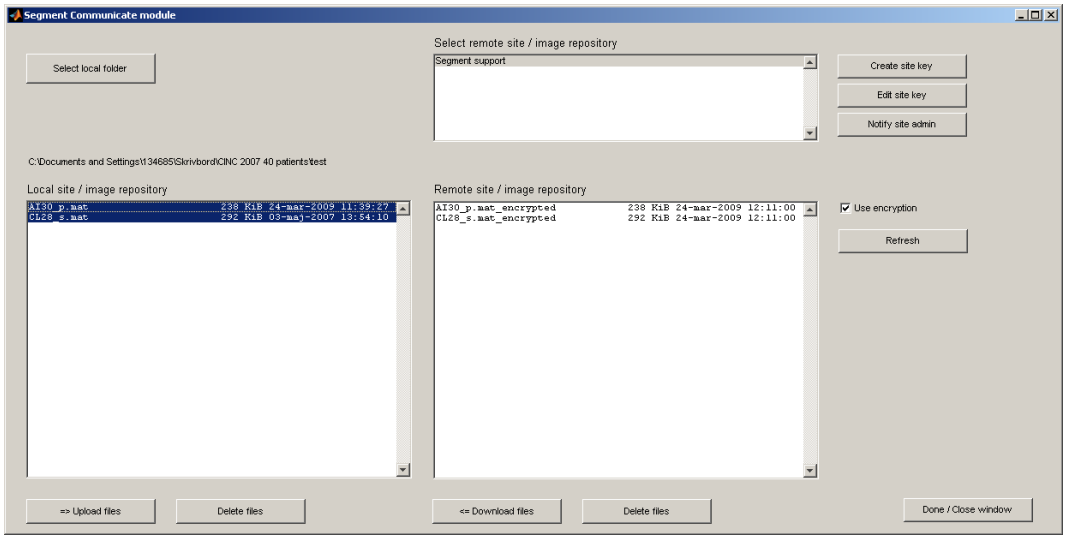



Figure 63: GUI for the communication module.

## 40.4 Edit site key

To edit a site key, just select Edit Site Key. This will bring up a dialog box similar to that one shown in Figure 61. Using this dialog box enables you to change all fields. Note, that you **need** to retype the password. Furthermore, also remember to resend the site key to your collaborators.

# 41 Report Sheet Generator Module

This functionality is only available in the clinical/commercial version of Segment. The patient report generator is a tool to generate reports of a study. The tool is started by the icon or under the Report menu. The graphical user interface is illustrated in Figure 64. Currently this functionality is still in a Beta stage and will be further integrated into the patient database.

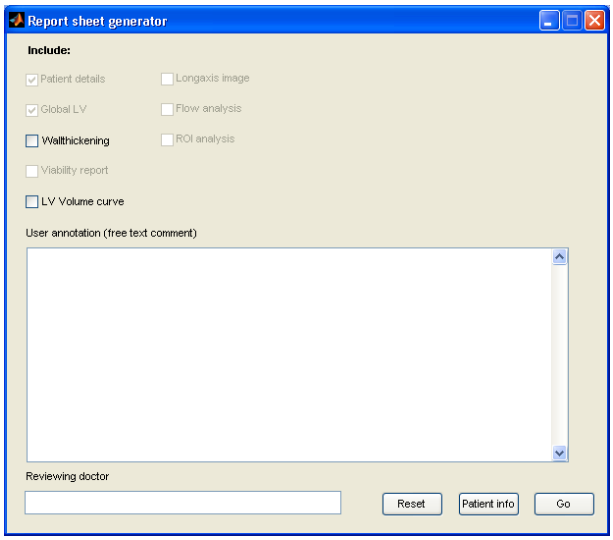



Figure 64: GUI for patient report generator.

The checkboxes are used to select what details that should be included in the report. There is one large text area where it is possible to enter textual reports about the study. This text is stored together with the segmentation. Another text field in the GUI is reporting doctor. Here you could type in the name of the doctor performing the analysis and the report. You could also leave the field empty and put in your signature in the printed report. The report is generated in `HTML` format and consists of up to five pages. Each paper can be printed and together this contains a detailed report of an exam.

- Patient details page, this page consists of patient details, the free text

textual comment, reviwing doctor.

- Global LV function, this page contains global LV parameters, and an image of the short axis stack in end-systole and in end-diastole with the delineation.
- Regional LV function, this page contains regional left ventricle analysis including a bulls eye plot.
- Viability report, this page contains information about viability analysis including a bulls-eye plot in the 17 segment model.
- Flow, this page contains information about flow measurements and analysis of valve insufficiencies.

# 42 Plugins

The functions described in this chapter is off label use and for investigational use only.

In Segment it is possible to create own plugins and extensions. This is further described in [12] and the Technical Manual. Currently there are two plugins that are shipped with the stand-alone version of Segment.

## 42.1 Image Loader Plugin

The image loader plugin is used to load diffrent kinds of images into segment. The plugin currently supports the following image formats.

- JPEG (*.jpg)
- PNG (*.png)
- TIFF (*.tif)

There are two diffrent ways of loading images in the image loader plugin. The first way, called Load single file, load a single image file in a new image stack. The second way, called Load files from directory, loads all files in a directory and places them in a single image stack. The images are ordered according to filename and placed in z-depth.

Some information, such as resolution, that exist in dicom files are not present in these general image formats. The image loader plugin will simply guess on default values for these values. Sometimes one can use the calibrate plugin to set the resolution to a correct value.

## 42.2 Calibrate Plugin

Sometimes the correct resolution for an image stack isn't known. However if one knows the area of some region of the image beforehand one can calculate the correct resolution. This plugin helps one do that.

When loading the plugin one is presented with a red square. By moving the corners of the square one can select the region. One is also presented with a input box where it's possible to enter the area of this region. When

pressing the ok button the plugin calculate the correct resolution and updates the image stack accordingly. Note that this plugin assumes isotrope images.

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